STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 113949

TO: Cynthia Wilder
Location: Rem 2a35
Thursday, February 12, 2004
Art Unit: 1637
Phone: 272-0791
Serial Number: 09 / 981606

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes

1139449

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Tuesday, February 10, 2004 9:23 AM
To: Wilder, Cynthia; STIC-Biotech/ChemLib
Subject: RE: Rush sequence search for 09/981606

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From: Wilder, Cynthia
Sent: Tuesday, February 10, 2004 9:09 AM
To: Chan, Christina
Subject: Rush sequence search for 09/981606

Ms. Chan,

I am requesting a rush sequence search and for interference of the following: 09981606. This case needs prompt attention.
Please forward your approval to STIC

Please provide a search of nucleotides 67-339 of SEQ ID NO: 1, wherein at position 193 and A is substituted for a T.

Please provide a search of nucleotides 700-850 of SEQ ID NO: 1, wherein a mutation is located at nucleotide 845.

Please provide a search of nucleotides 4652-4915 and nucleotides 6494-6927 of SEQ ID NO: 27.

Thank you

Cynthia B. Wilder, Ph.D.
United States Patent and TradeMark Office
Carlyle Remson 2A35
(571) 272-0791

2C18

Searcher: [signature]
Phone: 22504
Location:
Date Picked Up: 2/10
Date Completed: 2/12
Searcher Prep/Review:
Clerical: 10
Online time: +20

TYPE OF SEARCH: ✓
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: ✓
WWW/Internet:
Other (specify):

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 15:39:52 ; Search time 49.5778 Seconds
(without alignments)
2430.473 Million cell updates/sec

Title: 09981606-1A_COPY_67_339
Perfect score: 273
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	271.4	99.4	1440	3	US-08-652-265-9	Sequence 9, Appli
2	271.4	99.4	1440	3	US-08-652-265-10	Sequence 10, Appl
3	271.4	99.4	1440	3	US-08-834-497A-9	Sequence 9, Appli
4	271.4	99.4	1440	3	US-08-834-497A-10	Sequence 10, Appl
5	271.4	99.4	1440	3	US-09-503-444A-9	Sequence 9, Appli
6	271.4	99.4	1440	3	US-09-503-444A-10	Sequence 10, Appl
7	271.4	99.4	2506	4	US-09-277-457-1	Sequence 1, Appli
8	271.4	99.4	2506	4	US-09-679-729-1	Sequence 1, Appli
9	269.8	98.8	1440	3	US-08-652-265-11	Sequence 11, Appl
10	269.8	98.8	1440	3	US-08-652-265-12	Sequence 12, Appl
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ALIGNMENTS

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RESULT 1
US-08-652-265-9
; Sequence 9, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "c")
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;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d2
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;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
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US-08-652-265-9

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  Best Local Similarity   99.6%;  Pred. No. 4.6e-82;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 2
US-08-652-265-10
; Sequence 10, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
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;    FEATURE:
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;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-10

  Query Match             99.4%;  Score 271.4;  DB 3;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 4.6e-82;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 3
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; Sequence 9, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       SOFTWARE:  FastSEQ for Windows Version 2.0b
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/834,497A
;       FILING DATE:  04-APR-1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/652,265
;       FILING DATE:  23-MAY-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/632,673
;       FILING DATE:  16-APR-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/630,912
;       FILING DATE:  04-APR-1996
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M.
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  8907-0056-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-493-4935
;       TELEFAX:  650-493-5556
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1440 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  222..1268
;     FEATURE:
;       NAME/KEY:  allele
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;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d2
;     FEATURE:
;       NAME/KEY:  allele
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;       OTHER INFORMATION:  /phenotype= "normal or wild-type
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;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d1
US-08-834-497A-9

  Query Match             99.4%;  Score 271.4;  DB 3;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 4.6e-82;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 4
US-08-834-497A-10
; Sequence 10, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
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;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
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; OTHER INFORMATION: /label= 24d1
US-08-834-497A-10

Query Match 99.4%; Score 271.4; DB 3; Length 1440;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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RESULT 5
US-09-503-444A-9
; Sequence 9, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(408, "c")
; OTHER INFORMATION: /phenotype= "normal or wild-type
; OTHER INFORMATION: (unaffected)"
; OTHER INFORMATION: /label= 24d2
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(414, "a")
; OTHER INFORMATION: /phenotype= "normal or wild-type
; OTHER INFORMATION: (unaffected)"
; OTHER INFORMATION: /label= 24d7
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(1066, "g")
; OTHER INFORMATION: /phenotype= "normal or wild-type
; OTHER INFORMATION: (unaffected)"
; OTHER INFORMATION: /label= 24d1
US-09-503-444A-9

Query Match 99.4%; Score 271.4; DB 3; Length 1440;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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RESULT 6
US-09-503-444A-10
; Sequence 10, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(1066, "a")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
; OTHER INFORMATION:
; OTHER INFORMATION: /label= 24d1
US-09-503-444A-10

Query Match 99.4%; Score 271.4; DB 3; Length 1440;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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RESULT 7
US-09-277-457-1
; Sequence 1, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Barry E.
; APPLICANT: Sawada-Hirai, Ritsuko
; APPLICANT: Barton, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERENCE: 10653/002001
; CURRENT APPLICATION NUMBER: US/09/277,457
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (0)...(0)
; OTHER INFORMATION: Missense mutation at nucleotide 314
US-09-277-457-1

Query Match 99.4%; Score 271.4; DB 4; Length 2506;
Best Local Similarity 99.6%; Pred. No. 6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 126

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 186

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 246

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        247 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 306

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        307 TGGACTATTATGGAAAATCACAACCACAGCAAG 339
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RESULT 8
US-09-679-729-1
; Sequence 1, Application US/09679729
; Patent No. 6509442
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Barry E.
; APPLICANT: Sawada-Hirai, Ritsuko
; APPLICANT: Barton, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERENCE: 24065-004 DIV
; CURRENT APPLICATION NUMBER: US/09/679,729
; CURRENT FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (0)...(0)

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;   OTHER INFORMATION: Missense mutation at nucleotide 314
US-09-679-729-1

  Query Match             99.4%;  Score 271.4;  DB 4;  Length 2506;
  Best Local Similarity   99.6%;  Pred. No. 6e-82;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db         67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 126

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        127 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 186

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Db        187 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 246

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 306

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        307 TGGACTATTATGGAAAATCACAACCACAGCAAG 339


RESULT 9
US-08-652-265-11
; Sequence 11, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-08-652-265-11

  Query Match             98.8%;  Score 269.8;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-81;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Db        408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 10
US-08-652-265-12
; Sequence 12, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  12:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
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;      NAME/KEY:  allele
;      LOCATION:  replace(408, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
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;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-12

  Query Match             98.8%;  Score 269.8;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-81;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Db        408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 11
US-08-834-497A-11
; Sequence 11, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-08-834-497A-11

  Query Match             98.8%;  Score 269.8;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-81;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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RESULT 12
US-08-834-497A-12
; Sequence 12, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
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;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-12

  Query Match             98.8%;  Score 269.8;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-81;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 13
US-09-503-444A-11
; Sequence 11, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-09-503-444A-11

  Query Match             98.8%;  Score 269.8;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-81;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Db        408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 14
US-09-503-444A-12
; Sequence 12, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-09-503-444A-12

  Query Match             98.8%;  Score 269.8;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-81;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Db        408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 15
US-08-652-265-1
; Sequence 1, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
```

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;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= "No. 6025130mal or wild-type (unaffected)
;      OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;      OTHER INFORMATION:  allele"
;    FEATURE:
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;      LOCATION:  140..7319
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;      LOCATION:  3852..3891
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;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;      OTHER INFORMATION:  allele (SEQ ID NO:41)"
;    FEATURE:
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;      OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
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;      LOCATION:  replace(3872, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
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;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-1

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  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Qy        251 TGGAAAATCACAACCACAGCAAG 273
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GenCore version 5.1.6

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Listing first 45 summaries

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SUMMARIES

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4	269.8	98.8	746	6	US-10-741-600-272	Sequence 272, App
5	269.8	98.8	746	8	US-60-524-882-114	Sequence 114, App
6	269.8	98.8	2009	1	PCT-US03-40978-266	Sequence 266, App
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9	269.8	98.8	2285	1	PCT-US03-40978-271	Sequence 271, App
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11	269.8	98.8	2285	8	US-60-524-882-113	Sequence 113, App
12	269.8	98.8	2398	1	PCT-US03-40978-270	Sequence 270, App
13	269.8	98.8	2398	6	US-10-741-600-270	Sequence 270, App
14	269.8	98.8	2398	8	US-60-524-882-111	Sequence 111, App
15	269.8	98.8	2440	1	PCT-US03-40978-261	Sequence 261, App
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17	269.8	98.8	2440	8	US-60-524-882-104	Sequence 104, App
18	269.8	98.8	2674	1	PCT-US03-40978-267	Sequence 267, App
19	269.8	98.8	2674	6	US-10-741-600-267	Sequence 267, App
20	269.8	98.8	2674	8	US-60-524-882-109	Sequence 109, App
21	269.8	98.8	2716	1	PCT-US03-40978-265	Sequence 265, App
22	269.8	98.8	2716	6	US-10-741-600-265	Sequence 265, App
23	269.8	98.8	2716	8	US-60-524-882-107	Sequence 107, App
24	261	95.6	21608	8	US-60-487-610-19486	Sequence 19486, A
25	259.8	95.2	21608	1	PCT-US03-40978-17631	Sequence 17631, A
26	259.8	95.2	21608	6	US-10-741-600-17631	Sequence 17631, A
27	259.8	95.2	21608	8	US-60-524-882-9174	Sequence 9174, Ap
28	212	77.7	676	8	US-60-487-610-486	Sequence 486, App
29	210.4	77.1	897	1	PCT-US03-40978-262	Sequence 262, App
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33	200.6	73.5	201	1	PCT-US03-40978-7447	Sequence 7447, Ap
34	200.6	73.5	201	1	PCT-US03-40978-7462	Sequence 7462, Ap
35	200.6	73.5	201	1	PCT-US03-40978-7480	Sequence 7480, Ap
36	200.6	73.5	201	1	PCT-US03-40978-7525	Sequence 7525, Ap
37	200.6	73.5	201	1	PCT-US03-40978-7543	Sequence 7543, Ap
38	200.6	73.5	201	1	PCT-US03-40978-7549	Sequence 7549, Ap
39	200.6	73.5	201	1	PCT-US03-40978-29714	Sequence 29714, A
40	200.6	73.5	201	6	US-10-741-600-7399	Sequence 7399, Ap
41	200.6	73.5	201	6	US-10-741-600-7447	Sequence 7447, Ap
42	200.6	73.5	201	6	US-10-741-600-7462	Sequence 7462, Ap
43	200.6	73.5	201	6	US-10-741-600-7480	Sequence 7480, Ap
44	200.6	73.5	201	6	US-10-741-600-7525	Sequence 7525, Ap
45	200.6	73.5	201	6	US-10-741-600-7543	Sequence 7543, Ap

ALIGNMENTS

RESULT 1
US-60-487-610-485
; Sequence 485, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 485
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-485

Query Match 99.3%; Score 271; DB 8; Length 1724;
Best Local Similarity 98.2%; Pred. No. 1.2e-84;
Matches 268; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 126

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 186

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 SATGAGWGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 246

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        247 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 306

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||:||||||||||||||||||||||||
Db        307 TGGACTAYTATGGAAAATCACAACCACAGCAAG 339
```

RESULT 2
US-60-487-610-487
; Sequence 487, Application US/60487610

```
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 487
;   LENGTH: 2285
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-487-610-487

  Query Match             99.3%;  Score 271;  DB 8;  Length 2285;
  Best Local Similarity   98.2%;  Pred. No. 1.3e-84;
  Matches  268;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 SATGAGWGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||:||||||||||||||||||||||||
Db        528 TGGACTAYTATGGAAAATCACAACCACAGCAAG 560


RESULT 3
PCT-US03-40978-272
; Sequence 272, Application PC/TUS0340978
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: PCT/US03/40978
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
;   LENGTH: 746
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-40978-272

  Query Match             98.8%;  Score 269.8;  DB 1;  Length 746;
  Best Local Similarity   97.1%;  Pred. No. 2.2e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||:||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:|||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 4
US-10-741-600-272
; Sequence 272, Application US/10741600
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
;   LENGTH: 746
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-272

  Query Match             98.8%;  Score 269.8;  DB 6;  Length 746;
  Best Local Similarity   97.1%;  Pred. No. 2.2e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||:||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:|||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 5
US-60-524-882-114
; Sequence 114, Application US/60524882
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001494
;  CURRENT APPLICATION NUMBER: US/60/524,882
;  CURRENT FILING DATE:  2003-11-26
;  NUMBER OF SEQ ID NOS: 46672
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114
;   LENGTH: 746
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

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US-60-524-882-114

  Query Match             98.8%;  Score 269.8;  DB 8;  Length 746;
  Best Local Similarity   97.1%;  Pred. No. 2.2e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||:||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:|||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 6
PCT-US03-40978-266
; Sequence 266, Application PC/TUS0340978
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: PCT/US03/40978
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 266
;   LENGTH: 2009
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-40978-266

  Query Match             98.8%;  Score 269.8;  DB 1;  Length 2009;
  Best Local Similarity   97.1%;  Pred. No. 3.3e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||:||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:|||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 7
US-10-741-600-266
; Sequence 266, Application US/10741600
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 266
;   LENGTH: 2009
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-266

  Query Match             98.8%;  Score 269.8;  DB 6;  Length 2009;
  Best Local Similarity   97.1%;  Pred. No. 3.3e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||:||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:|||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 8
US-60-524-882-108
; Sequence 108, Application US/60524882
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001494
;  CURRENT APPLICATION NUMBER: US/60/524,882
;  CURRENT FILING DATE:  2003-11-26
;  NUMBER OF SEQ ID NOS: 46672
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 108
;   LENGTH: 2009
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-524-882-108

  Query Match             98.8%;  Score 269.8;  DB 8;  Length 2009;
  Best Local Similarity   97.1%;  Pred. No. 3.3e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||:||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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              :|:|||:|||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 9
PCT-US03-40978-271
; Sequence 271, Application PC/TUS0340978
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: PCT/US03/40978
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 271
;   LENGTH: 2285
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-40978-271

  Query Match             98.8%;  Score 269.8;  DB 1;  Length 2285;
  Best Local Similarity   97.1%;  Pred. No. 3.5e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||||:||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:|||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 10
US-10-741-600-271
; Sequence 271, Application US/10741600
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 271
;   LENGTH: 2285
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-271

  Query Match             98.8%;  Score 269.8;  DB 6;  Length 2285;
  Best Local Similarity   97.1%;  Pred. No. 3.5e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||||:||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:|||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 11
US-60-524-882-113
; Sequence 113, Application US/60524882
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001494
;  CURRENT APPLICATION NUMBER: US/60/524,882
;  CURRENT FILING DATE:  2003-11-26
;  NUMBER OF SEQ ID NOS: 46672
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113
;   LENGTH: 2285
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-524-882-113

  Query Match             98.8%;  Score 269.8;  DB 8;  Length 2285;
  Best Local Similarity   97.1%;  Pred. No. 3.5e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||||:||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:|||||||||||||||||:||||||||||||||||||||||||||||||||||||
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Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 12
PCT-US03-40978-270
; Sequence 270, Application PC/TUS0340978
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; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: PCT/US03/40978
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 270
;   LENGTH: 2398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-40978-270

  Query Match             98.8%;  Score 269.8;  DB 1;  Length 2398;
  Best Local Similarity   97.1%;  Pred. No. 3.5e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||:||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 13
US-10-741-600-270
; Sequence 270, Application US/10741600
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 270
;   LENGTH: 2398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-270

  Query Match             98.8%;  Score 269.8;  DB 6;  Length 2398;
  Best Local Similarity   97.1%;  Pred. No. 3.5e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 14
US-60-524-882-111
; Sequence 111, Application US/60524882
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001494
;  CURRENT APPLICATION NUMBER: US/60/524,882
;  CURRENT FILING DATE:  2003-11-26
;  NUMBER OF SEQ ID NOS: 46672
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
;   LENGTH: 2398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-524-882-111

  Query Match             98.8%;  Score 269.8;  DB 8;  Length 2398;
  Best Local Similarity   97.1%;  Pred. No. 3.5e-84;
  Matches  265;  Conservative    8;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:||||||||||||||||:||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 15
PCT-US03-40978-261
; Sequence 261, Application PC/TUS0340978
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: PCT/US03/40978
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261
;   LENGTH: 2440
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-40978-261
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Query Match 98.8%; Score 269.8; DB 1; Length 2440;
Best Local Similarity 97.1%; Pred. No. 3.6e-84;
Matches 265; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCAYGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||:|||||||||||||||:||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACRTGGATGACCAGCTGTTCRTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              :|:|||:|||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        408 SAYGAGWGTCGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAASGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	273	100.0	1440	46	US-10-138-888-77	Sequence 77, Appl
2	271.4	99.4	1045	82	US-60-278-232-6940	Sequence 6940, Ap
3	271.4	99.4	1440	13	US-08-834-497-9	Sequence 9, Appli
4	271.4	99.4	1440	13	US-08-834-497-10	Sequence 10, Appl

5	271.4	99.4	1440	21	US-09-497-957-9	Sequence 9, Appli
6	271.4	99.4	1440	21	US-09-497-957-10	Sequence 10, Appl
7	271.4	99.4	1440	46	US-10-138-888-9	Sequence 9, Appli
8	271.4	99.4	1440	46	US-10-138-888-10	Sequence 10, Appl
9	271.4	99.4	1724	47	US-10-170-235-26715	Sequence 26715, A
10	271.4	99.4	2285	47	US-10-170-235-27072	Sequence 27072, A
11	271.4	99.4	2506	43	US-09-981-606-1	Sequence 1, Appli
12	271.4	99.4	2619	32	US-09-724-676-18074	Sequence 18074, A
13	271.4	99.4	2619	32	US-09-724-676A-18074	Sequence 18074, A
14	271.4	99.4	2717	40	US-09-949-016-1180	Sequence 1180, Ap
15	271.4	99.4	2727	40	US-09-949-016-64	Sequence 64, Appl
16	271.4	99.4	2727	102	US-60-474-850-46	Sequence 46, Appl
17	271.4	99.4	2739	14	US-08-920-559-1	Sequence 1, Appli
18	271.4	99.4	2739	14	US-08-920-559A-1	Sequence 1, Appli
19	271.4	99.4	2777	32	US-09-724-676-18068	Sequence 18068, A
20	271.4	99.4	2777	32	US-09-724-676A-18068	Sequence 18068, A
21	271.4	99.4	2819	32	US-09-724-676-18073	Sequence 18073, A
22	271.4	99.4	2819	32	US-09-724-676A-18073	Sequence 18073, A
23	271	99.3	1724	100	US-60-452-680-6251	Sequence 6251, Ap
24	271	99.3	1724	100	US-60-453-050-3472	Sequence 3472, Ap
25	271	99.3	1724	100	US-60-453-135-3472	Sequence 3472, Ap
26	271	99.3	1724	100	US-60-455-444-1579	Sequence 1579, Ap
27	271	99.3	1724	101	US-60-465-241-1579	Sequence 1579, Ap
28	271	99.3	1724	101	US-60-466-412-3472	Sequence 3472, Ap
29	271	99.3	2285	100	US-60-452-680-6253	Sequence 6253, Ap
30	271	99.3	2285	100	US-60-453-050-3474	Sequence 3474, Ap
31	271	99.3	2285	100	US-60-453-135-3474	Sequence 3474, Ap
32	271	99.3	2285	100	US-60-455-444-1581	Sequence 1581, Ap
33	271	99.3	2285	101	US-60-465-241-1581	Sequence 1581, Ap
34	271	99.3	2285	101	US-60-466-412-3474	Sequence 3474, Ap
35	269.8	98.8	400	18	US-09-274-861-1761	Sequence 1761, Ap
36	269.8	98.8	400	38	US-09-915-738-1761	Sequence 1761, Ap
37	269.8	98.8	1440	13	US-08-834-497-11	Sequence 11, Appl
38	269.8	98.8	1440	13	US-08-834-497-12	Sequence 12, Appl
39	269.8	98.8	1440	21	US-09-497-957-11	Sequence 11, Appl
40	269.8	98.8	1440	21	US-09-497-957-12	Sequence 12, Appl
41	269.8	98.8	1440	46	US-10-138-888-11	Sequence 11, Appl
42	269.8	98.8	1440	46	US-10-138-888-12	Sequence 12, Appl
43	263	96.3	10825	46	US-10-138-888-79	GENERAL INFORMA
44	261.4	95.8	601	40	US-09-949-016-18793	Sequence 18793, A
45	261.4	95.8	601	40	US-09-949-016-41388	Sequence 41388, A

ALIGNMENTS

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RESULT 1
US-10-138-888-77
; Sequence 77, Application US/10138888
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 77:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1440 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  222..1268
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(414, "t")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d7
;        SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-138-888-77

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  Matches  273;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 2
US-60-278-232-6940
; Sequence 6940, Application US/60278232
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION:  Polynucleotide Sequence Databases, and Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms Identified Thereby
;  FILE REFERENCE: GX-0011 P
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;  CURRENT APPLICATION NUMBER: US/60/278,232
;  CURRENT FILING DATE:  2001-03-30
;  NUMBER OF SEQ ID NOS: 12,557
;  SOFTWARE: PERL Program
; SEQ ID NO 6940
;   LENGTH: 1045
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 333732.1
US-60-278-232-6940

  Query Match             99.4%;  Score 271.4;  DB 82;  Length 1045;
  Best Local Similarity   99.6%;  Pred. No. 2.3e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        103 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 162

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        163 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 222

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        283 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 342

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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RESULT 3
US-08-834-497-9
; Sequence 9, Application US/08834497
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000520US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 326-2400
;      TELEFAX:  (650) 326-2422
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(414, "a")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d7
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "g")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497-9

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  Best Local Similarity   99.6%;  Pred. No. 2.6e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 4
US-08-834-497-10
; Sequence 10, Application US/08834497
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
```

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;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000520US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 326-2400
;      TELEFAX:  (650) 326-2422
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497-10

  Query Match             99.4%;  Score 271.4;  DB 13;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 2.6e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 5
US-09-497-957-9
; Sequence 9, Application US/09497957
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/497,957
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497
;      FILING DATE:  04-APR-1997
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
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;       LOCATION:  replace(408, "c")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d2
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(414, "a")
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;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d7
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(1066, "g")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d1
US-09-497-957-9

  Query Match             99.4%;  Score 271.4;  DB 21;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 2.6e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 6
US-09-497-957-10
; Sequence 10, Application US/09497957
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/497,957
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497
;      FILING DATE:  04-APR-1997
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-09-497-957-10

  Query Match             99.4%;  Score 271.4;  DB 21;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 2.6e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 7
US-10-138-888-9
; Sequence 9, Application US/10138888
;  GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
```

```
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1440 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  222..1268
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(408, "c")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d2
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(414, "a")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d7
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(1066, "g")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-138-888-9

  Query Match             99.4%;  Score 271.4;  DB 46;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 2.6e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 8
US-10-138-888-10
; Sequence 10, Application US/10138888
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1440 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  222..1268
;       FEATURE:
;            NAME/KEY:  allele
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;             LOCATION:  replace(1066, "a")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d1
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-138-888-10

  Query Match             99.4%;  Score 271.4;  DB 46;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 2.6e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 9
US-10-170-235-26715
; Sequence 26715, Application US/10170235
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
;  TITLE OF INVENTION:  TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
;  FILE REFERENCE: CL001380
;  CURRENT APPLICATION NUMBER: US/10/170,235
;  CURRENT FILING DATE:  2003-03-17
;  NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 26715
;   LENGTH: 1724
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-170-235-26715

  Query Match             99.4%;  Score 271.4;  DB 47;  Length 1724;
  Best Local Similarity   99.6%;  Pred. No. 2.8e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 126

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 186

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 246

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 306

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        307 TGGACTATTATGGAAAATCACAACCACAGCAAG 339


RESULT 10
US-10-170-235-27072
; Sequence 27072, Application US/10170235
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
;  TITLE OF INVENTION:  TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
;  FILE REFERENCE: CL001380
;  CURRENT APPLICATION NUMBER: US/10/170,235
;  CURRENT FILING DATE:  2003-03-17
;  NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 27072
;   LENGTH: 2285
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-170-235-27072

  Query Match             99.4%;  Score 271.4;  DB 47;  Length 2285;
  Best Local Similarity   99.6%;  Pred. No. 3.1e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 11
US-09-981-606-1
; Sequence 1, Application US/09981606
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg et al.
;  TITLE OF INVENTION: Mutations associated with iron disorders
;  FILE REFERENCE: 24065-004CON
;  CURRENT APPLICATION NUMBER: US/09/981,606
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2506
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-981-606-1

  Query Match             99.4%;  Score 271.4;  DB 43;  Length 2506;
  Best Local Similarity   99.6%;  Pred. No. 3.2e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 126

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 186
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Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Db        187 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 246

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 306

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        307 TGGACTATTATGGAAAATCACAACCACAGCAAG 339


RESULT 12
US-09-724-676-18074
; Sequence 18074, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18074
;   LENGTH: 2619
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676-18074

  Query Match             99.4%;  Score 271.4;  DB 32;  Length 2619;
  Best Local Similarity   99.6%;  Pred. No. 3.3e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 13
US-09-724-676A-18074
; Sequence 18074, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18074
;   LENGTH: 2619
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676A-18074

  Query Match             99.4%;  Score 271.4;  DB 32;  Length 2619;
  Best Local Similarity   99.6%;  Pred. No. 3.3e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 14
US-09-949-016-1180
; Sequence 1180, Application US/09949016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1180
;   LENGTH: 2717
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1180

  Query Match             99.4%;  Score 271.4;  DB 40;  Length 2717;
  Best Local Similarity   99.6%;  Pred. No. 3.3e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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RESULT 15
US-09-949-016-64
; Sequence 64, Application US/09949016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
;   LENGTH: 2727
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-64

  Query Match             99.4%;  Score 271.4;  DB 40;  Length 2727;
  Best Local Similarity   99.6%;  Pred. No. 3.4e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


Search completed: February 11, 2004, 20:55:16
Job time : 2227.5 secs
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 15:39:51 ; Search time 1634.78 Seconds
(without alignments)
6831.698 Million cell updates/sec

Title: 09981606-1A_COPY_67_339
Perfect score: 273
Sequence: 1 cgcttgctgcgttcacactc.....aaaatcacaaccacagcaag 273

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
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14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		271.4	99.4	735	9	AF115264	AF115264 Homo sapi
2		271.4	99.4	804	9	AF149804	AF149804 Homo sapi
3		271.4	99.4	1045	9	AF079407	AF079407 Homo sapi
4		271.4	99.4	1073	9	HSA249337	AJ249337 Homo sapi
5		271.4	99.4	1200	9	AF115265	AF115265 Homo sapi
6		271.4	99.4	1317	6	AX407339	AX407339 Sequence
7		271.4	99.4	1440	6	AR117793	AR117793 Sequence
8		271.4	99.4	1440	6	AR117794	AR117794 Sequence
9		271.4	99.4	1440	6	AR149463	AR149463 Sequence
10		271.4	99.4	1440	6	AR149464	AR149464 Sequence
11		271.4	99.4	1885	9	AF144242	AF144242 Homo sapi
12		271.4	99.4	2506	6	AR199238	AR199238 Sequence
13		271.4	99.4	2506	6	AR275757	AR275757 Sequence
14		271.4	99.4	2727	9	HSU60319	U60319 Homo sapien
15		269.8	98.8	1440	6	AR117795	AR117795 Sequence
16		269.8	98.8	1440	6	AR117796	AR117796 Sequence
17		269.8	98.8	1440	6	AR149465	AR149465 Sequence
18		269.8	98.8	1440	6	AR149466	AR149466 Sequence
19		266.6	97.7	987	9	AF150664	AF150664 Homo sapi
20		261.4	95.8	874	9	HSHLAH2	Y09800 H.sapiens H
21		261.4	95.8	5982	6	AX701831	AX701831 Sequence
22		261.4	95.8	10825	6	AR117789	AR117789 Sequence
23		261.4	95.8	10825	6	AR117790	AR117790 Sequence
24		261.4	95.8	10825	6	AR149459	AR149459 Sequence
25		261.4	95.8	10825	6	AR149460	AR149460 Sequence
26	c	261.4	95.8	11214	9	AF447807	AF447807 Pan trogl
27		261.4	95.8	12146	6	AR199263	AR199263 Sequence
28		261.4	95.8	12146	6	AR275782	AR275782 Sequence
29		261.4	95.8	12146	9	HSHFE	Z92910 Homo sapien
30	c	261.4	95.8	193752	2	AL359892	AL359892 Homo sapi
31	c	261.4	95.8	235033	6	BD084121	BD084121 Polymorph
32	c	261.4	95.8	237326	6	BD084122	BD084122 Polymorph
33		261.4	95.8	246240	6	AR036572	AR036572 Sequence
34		261.4	95.8	246240	6	AR036573	AR036573 Sequence
35		261.4	95.8	246240	6	AR036574	AR036574 Sequence
36	c	261.4	95.8	246282	9	HSU91328	U91328 Human hered
37		259.8	95.2	10825	6	AR117791	AR117791 Sequence
38		259.8	95.2	10825	6	AR117792	AR117792 Sequence
39		259.8	95.2	10825	6	AR149461	AR149461 Sequence
40		259.8	95.2	10825	6	AR149462	AR149462 Sequence
41		204	74.7	560	9	AF144243	AF144243 Homo sapi
42		192.4	70.5	1280	9	HSA249335	AJ249335 Homo sapi
43		186.6	68.4	1319	4	AY007544	AY007544 Rhinocero
44		186.6	68.4	1320	4	AY007543	AY007543 Dicerorhi
45		185.4	67.9	1320	4	AY007541	AY007541 Ceratothe

ALIGNMENTS

RESULT 1
AF115264
LOCUS AF115264 735 bp mRNA linear PRI 07-MAY-2001
DEFINITION Homo sapiens hemochromatosis splice variant delE3-7 (HFE) mRNA, complete cds.
ACCESSION AF115264
VERSION AF115264.1 GI:11094312
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 735)
AUTHORS Thenie,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y., David,V. and Mosser,J.

```
  TITLE     The HFE gene undergoes alternate splicing processes
  JOURNAL   Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
  MEDLINE   20448010
   PUBMED   11001625
REFERENCE   2  (bases 1 to 735)
  AUTHORS   Thenie,A., Orhant,M. and Mosser,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1998) UPR 41 CNRS, Faculte de Medecine, 2, av du
            Pr. Bernard, Rennes 35043, France
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p22"
     gene            1. .735
                     /gene="HFE"
     CDS             7. .492
                     /gene="HFE"
                     /codon_start=1
                     /product="hemochromatosis splice variant delE3-7"
                     /protein_id="AAG29571.1"
                     /db_xref="GI:11094313"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
                     SLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDF
                     WTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQVLQDTIYSSEVSSLGIK
                     F"
BASE COUNT      203 a    147 c    168 g    217 t
ORIGIN

  Query Match           99.4%;  Score 271.4;  DB 9;  Length 735;
  Best Local Similarity  99.6%;  Pred. No. 3.9e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 132

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 192

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 252

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 312

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        313 TGGACTATTATGGAAAATCACAACCACAGCAAG 345


RESULT 2
AF149804
LOCUS       AF149804                804 bp    mRNA    linear   PRI 07-MAY-2001
DEFINITION  Homo sapiens hemochromatosis protein splice variant 562-878del
            (HFE) mRNA, complete cds.
ACCESSION   AF149804
VERSION     AF149804.1  GI:11093523
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 804)
  AUTHORS   Thenie,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y.,
            David,V. and Mosser,J.
  TITLE     The HFE gene undergoes alternate splicing processes
  JOURNAL   Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
  MEDLINE   20448010
   PUBMED   11001625
REFERENCE   2  (bases 1 to 804)
  AUTHORS   Thenie,A., Orhant,M., Gicquel,I. and Mosser,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAY-1999) Faculte de Medecine, UPR 41 CNRS, 2 Avenue
            du Pr Leon Bernard, Rennes Cedex 35043, France
FEATURES             Location/Qualifiers
     source          1. .804
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p22"
     gene            1. .804
                     /gene="HFE"
     CDS             45. .773
                     /gene="HFE"
                     /codon_start=1
                     /product="hemochromatosis protein splice variant
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                     /protein_id="AAG29342.1"
                     /db_xref="GI:11093524"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
                     SLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDF
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                     WITLAVPPEEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIGVIRGIAVFVVILFIGI
                     LFIILRKRQGSRGAMGHYVLAERE"
BASE COUNT      181 a    199 c    233 g    191 t
ORIGIN

  Query Match           99.4%;  Score 271.4;  DB 9;  Length 804;
  Best Local Similarity  99.6%;  Pred. No. 3.9e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 170

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 230

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 290

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 350

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        351 TGGACTATTATGGAAAATCACAACCACAGCAAG 383


RESULT 3
AF079407
LOCUS       AF079407                1045 bp    mRNA    linear   PRI 18-MAR-1999
DEFINITION  Homo sapiens hemochromatosis splice variant del14E4 (HFE) mRNA,
            complete cds.
ACCESSION   AF079407
VERSION     AF079407.1  GI:3695106
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1045)
  AUTHORS   Rhodes,D.A. and Trowsdale,J.
  TITLE     Alternate splice variants of the hemochromatosis gene Hfe
  JOURNAL   Immunogenetics 49 (4), 357-359 (1999)
  MEDLINE   99180629
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   PUBMED   10079302
REFERENCE   2  (bases 1 to 1045)
  AUTHORS   Rhodes,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1998) Immunology, University of Cambridge, Tennis
            Court Road, Cambridge CB2 1QP, UK
FEATURES             Location/Qualifiers
     source          1. .1045
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p22.1"
     gene            1. .1045
                     /gene="HFE"
     CDS             37. .1041
                     /gene="HFE"
                     /codon_start=1
                     /product="hemochromatosis splice variant del14E4"
                     /protein_id="AAC62646.1"
                     /db_xref="GI:3695107"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
                     SLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDF
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                     RAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVTTLRCRALNYYP
                     QNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLD
                     QPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFIILRKRQGSRGAMGHYVLAERE
                     "
BASE COUNT      243 a    259 c    314 g    229 t
ORIGIN
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Query Match 99.4%; Score 271.4; DB 9; Length 1045;
Best Local Similarity 99.6%; Pred. No. 4e-76;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 162

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 222

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 282

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 342

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        343 TGGACTATTATGGAAAATCACAACCACAGCAAG 375
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```
RESULT 4
HSA249337
LOCUS       HSA249337              1073 bp    mRNA    linear   PRI 04-SEP-2001
DEFINITION  Homo sapiens mRNA for hemochromatosis protein (HFE gene) splice
            variant 3.
ACCESSION   AJ249337
VERSION     AJ249337.1  GI:15485422
KEYWORDS    alternative splicing; hemochromatosis protein; HFE gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   OIiva,R. and Sanchez,M.
  TITLE     Identification of different alternative splicing forms of the HFE
            gene
  JOURNAL   Unpublished
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REFERENCE   2  (bases 1 to 1073)
  AUTHORS   Oliva,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-SEP-1999) Oliva R., Faculty of Medicine and Clinic
            Hospital, Human Genome Research Group, Casanova 143, 08036, SPAIN
FEATURES             Location/Qualifiers
     source          1. .1073
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                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p22"
                     /cell_line="HepG2"
     gene            1. .1073
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     CDS             161. .931
                     /gene="HFE"
                     /function="iron metabolism"
                     /note="alternative splicing form wit deletion of complete
                     exon 3"
                     /codon_start=1
                     /evidence=experimental
                     /product="hemochromatosis protein"
                     /protein_id="CAC67794.1"
                     /db_xref="GI:15485423"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
                     SLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDF
                     WTIMENHNHSKVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFE
                     PKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIGVI
                     SGIAVFVVILFIGILFIILRKRQGSRGAMGHYVLAERE"
BASE COUNT      250 a    264 c    295 g    264 t
ORIGIN
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Query Match 99.4%; Score 271.4; DB 9; Length 1073;
Best Local Similarity 99.6%; Pred. No. 4e-76;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 286

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 346

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 406

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 466

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        467 TGGACTATTATGGAAAATCACAACCACAGCAAG 499
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```
RESULT 5
AF115265
LOCUS       AF115265               1200 bp    mRNA    linear   PRI 07-MAY-2001
DEFINITION  Homo sapiens hemochromatosis termination variant terE6 (HFE) mRNA,
            complete cds.
ACCESSION   AF115265
VERSION     AF115265.1  GI:11094314
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1200)
  AUTHORS   Thenie,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y.,
            David,V. and Mosser,J.
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  TITLE     The HFE gene undergoes alternate splicing processes
  JOURNAL   Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
  MEDLINE   20448010
   PUBMED   11001625
REFERENCE   2  (bases 1 to 1200)
  AUTHORS   Thenie,A., Orhant,M. and Mosser,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1998) UPR 41 CNRS, Faculte de Medecine, 2, av du
            Pr. Bernard, Rennes 35043, France
FEATURES             Location/Qualifiers
     source          1. .1200
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p22"
     gene            1. .1200
                     /gene="HFE"
     CDS             12. .1058
                     /gene="HFE"
                     /codon_start=1
                     /product="hemochromatosis termination variant terE6"
                     /protein_id="AAG29572.1"
                     /db_xref="GI:11094315"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
                     SLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDF
                     WTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEP
                     RAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTS
                     SVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGE
                     EQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFIILRKRQG
                     SRGAMGHYVLAERE"
BASE COUNT      298 a    290 c    346 g    266 t
ORIGIN

  Query Match             99.4%;  Score 271.4;  DB 9;  Length 1200;
  Best Local Similarity   99.6%;  Pred. No. 4e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 137

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 197

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 257

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 317

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        318 TGGACTATTATGGAAAATCACAACCACAGCAAG 350


RESULT 6
AX407339
LOCUS       AX407339               1317 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 1 from Patent WO0224929.
ACCESSION   AX407339
VERSION     AX407339.1  GI:21440046
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ehrlich,R., Rotem-Yehudar,R. and Laham,N.
  TITLE     A soluble beta 2 microglobulin (beta2m)/hfe monochain for
            biotechnological and therapeutic applications
  JOURNAL   Patent: WO 0224929-A 1 28-MAR-2002;
            Ramot University Authority for Applied Research & Industrial Dev
            LTD. (IL)
FEATURES             Location/Qualifiers
     source          1. .1317
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"
     CDS             1. .1317
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD35231.1"
                     /db_xref="GI:21440047"
                     /translation="MSRSVALAVLALLSLSGLEAIQRTPKIQVYSRHPAENGKSNFLN
                     CYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRV
                     NHVTLSQPKIVKWDRDMGGGGSGGGGSGGGGSRLLRSHSLHYLFMGASEQDLGLSLFE
                     ALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDFWTIM
                     ENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWP
                     TKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTSSVTT
                     LRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRY
                     TCQVEHPGLDQPLIVIWGLESRGPFEQKLISEEDLNMHTGHHHHHH"
BASE COUNT      320 a    325 c    367 g    305 t
ORIGIN

  Query Match             99.4%;  Score 271.4;  DB 6;  Length 1317;
  Best Local Similarity   99.6%;  Pred. No. 4e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 462

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 522

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 582

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 642

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        643 TGGACTATTATGGAAAATCACAACCACAGCAAG 675


RESULT 7
AR117793
LOCUS       AR117793               1440 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 9 from patent US 6140305.
ACCESSION   AR117793
VERSION     AR117793.1  GI:14098699
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1440)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 9 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .1440
                     /organism="unknown"
BASE COUNT      347 a    355 c    407 g    331 t
ORIGIN

  Query Match             99.4%;  Score 271.4;  DB 6;  Length 1440;
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  Best Local Similarity   99.6%;  Pred. No. 4.1e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 8
AR117794
LOCUS       AR117794               1440 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 10 from patent US 6140305.
ACCESSION   AR117794
VERSION     AR117794.1  GI:14098700
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1440)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 10 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .1440
                     /organism="unknown"
BASE COUNT      348 a    355 c    406 g    331 t
ORIGIN

  Query Match            99.4%;  Score 271.4;  DB 6;  Length 1440;
  Best Local Similarity  99.6%;  Pred. No. 4.1e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 9
AR149463
LOCUS       AR149463               1440 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 9 from patent US 6228594.
ACCESSION   AR149463
VERSION     AR149463.1  GI:15114054
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1440)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 9 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .1440
                     /organism="unknown"
BASE COUNT      347 a    355 c    407 g    331 t
ORIGIN

  Query Match            99.4%;  Score 271.4;  DB 6;  Length 1440;
  Best Local Similarity  99.6%;  Pred. No. 4.1e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 10
AR149464
LOCUS       AR149464               1440 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 10 from patent US 6228594.
ACCESSION   AR149464
VERSION     AR149464.1  GI:15114055
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1440)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 10 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .1440
                     /organism="unknown"
BASE COUNT      348 a    355 c    406 g    331 t
ORIGIN

  Query Match            99.4%;  Score 271.4;  DB 6;  Length 1440;
  Best Local Similarity  99.6%;  Pred. No. 4.1e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347
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Qy          61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy         121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
               |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy         181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy         241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
               |||||||||||||||||||||||||||||||||
Db         528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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RESULT 11
AF144242
LOCUS       AF144242               1885 bp    mRNA    linear   PRI 07-MAY-2001
DEFINITION  Homo sapiens hemochromatosis splice variant delE3 mRNA, complete
            cds.
ACCESSION   AF144242
VERSION     AF144242.1  GI:11094324
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1885)
  AUTHORS   Thenie,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y.,
            David,V. and Mosser,J.
  TITLE     The HFE gene undergoes alternate splicing processes
  JOURNAL   Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
  MEDLINE   20448010
   PUBMED   11001625
REFERENCE   2  (bases 1 to 1885)
  AUTHORS   Thenie,A., Orhant,M., Gicquel,I. and Mosser,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-1999) Faculte de Medecine, UPR41 CNRS, 2 Avenue
            du Pr. Leon Bernard, Rennes Cedex 35043, France
FEATURES             Location/Qualifiers
     source          1. .1885
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p22"
     gene            1. .1885
                     /gene="HFE"
     CDS             124. .894
                     /gene="HFE"
                     /codon_start=1
                     /product="hemochromatosis splice variant delE3"
                     /protein_id="AAG29577.1"
                     /db_xref="GI:11094325"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
                     SLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDF
                     WTIMENHNHSKVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFE
                     PKDALPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIGVI
                     SGIAVFVVILFIGILFIILRKRQGSRGAVGHYVLAERE"
BASE COUNT      453 a    442 c    458 g    532 t
ORIGIN

  Query Match            99.4%;  Score 271.4;  DB 9;  Length 1885;
  Best Local Similarity  99.6%;  Pred. No. 4.1e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         190 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 249
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Qy          61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         250 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 309

Qy         121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
               |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         310 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 369

Qy         181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         370 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 429

Qy         241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
               |||||||||||||||||||||||||||||||||
Db         430 TGGACTATTATGGAAAATCACAACCACAGCAAG 462
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RESULT 12
AR199238
LOCUS       AR199238               2506 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1 from patent US 6355425.
ACCESSION   AR199238
VERSION     AR199238.1  GI:20249312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2506)
  AUTHORS   Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.
  TITLE     Mutations associated with iron disorders
  JOURNAL   Patent: US 6355425-A 1 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .2506
                     /organism="unknown"
BASE COUNT      648 a    552 c    596 g    710 t
ORIGIN

  Query Match            99.4%;  Score 271.4;  DB 6;  Length 2506;
  Best Local Similarity  99.6%;  Pred. No. 4.2e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 126

Qy          61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         127 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 186

Qy         121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
               |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         187 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 246

Qy         181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         247 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 306

Qy         241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
               |||||||||||||||||||||||||||||||||
Db         307 TGGACTATTATGGAAAATCACAACCACAGCAAG 339
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RESULT 13
AR275757
LOCUS       AR275757               2506 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6509442.
ACCESSION   AR275757
VERSION     AR275757.1  GI:29709314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2506)
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  AUTHORS   Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.
  TITLE     Mutations associated with iron disorders
  JOURNAL   Patent: US 6509442-A 1 21-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .2506
                     /organism="unknown"
BASE COUNT      648 a    552 c    596 g    710 t
ORIGIN

  Query Match             99.4%;  Score 271.4;  DB 6;  Length 2506;
  Best Local Similarity   99.6%;  Pred. No. 4.2e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db         67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 126

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        187 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 246

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        247 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 306

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        307 TGGACTATTATGGAAAATCACAACCACAGCAAG 339


RESULT 14
HSU60319
LOCUS       HSU60319                 2727 bp    mRNA    linear   PRI 29-OCT-1997
DEFINITION  Homo sapiens haemochromatosis protein (HLA-H) mRNA, complete cds.
ACCESSION   U60319
VERSION     U60319.1  GI:1469789
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2727)
  AUTHORS   Feder,J.N., Gnirke,A., Thomas,W., Tsuchihashi,Z., Ruddy,D.A.,
            Basava,A., Dormishian,F., Domingo,R., Ellis,M.C., Fullan,A.,
            Hinton,L.M., Jones,N.L., Kimmel,B.E., Kronmal,G.S., Lauer,P.,
            Lee,V.K., Loeb,D.B., Mapa,F., McClelland,E., Meyer,N.C.,
            Mintier,G.A., Moeller,N., Moore,T., Morkang,E., Prass,C.E.,
            Quintana,L., Stranes,S.M., Schatzman,R.C., Brunke,K.J.,
            Drayna,D.T., Risch,N.J., Bacon,B.R. and Wolff,R.K.
  TITLE     A novel MHC class I-like gene is mutated in patients with
            hereditary haemochromatosis
  JOURNAL   Nat. Genet. 13 (4), 399-408 (1996)
  MEDLINE   96331279
   PUBMED   8696333
REFERENCE   2  (bases 1 to 2727)
  AUTHORS   Feder,J.N., Gnirke,A., Thomas,W., Tsuchihashi,Z., Ruddy,D.A.,
            Basava,A., Dormishian,F., Domingo,R., Ellis,M.C., Fullan,A.,
            Hinton,L.M., Jones,N.L., Kimmel,B.E., Kronmal,G.S., Lauer,P.,
            Lee,V.K., Loeb,D.B., Mapa,F., McClelland,E., Meyer,N.C.,
            Mintier,G.A., Moeller,N., Moore,T., Morkang,E., Prass,C.E.,
            Quintana,L., Stranes,S.M., Schatzman,R.C., Brunke,K.J.,
            Drayna,D.T., Risch,N.J., Bacon,B.R. and Wolff,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUN-1996) Mercator Genetics, 4040 Campbell Ave.,
            Menlo Park, CA 94025, USA
FEATURES             Location/Qualifiers
     source          1. .2727
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                     /map="6p21.3"
     gene            1. .2727
                     /gene="HLA-H"
                     /note="synonym: HFE"
     CDS             222. .1268
                     /gene="HLA-H"
                     /codon_start=1
                     /product="haemochromatosis protein"
                     /protein_id="AAC51823.1"
                     /db_xref="GI:1469790"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
                     SLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDF
                     WTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEP
                     RAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTS
                     SVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGE
                     EQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFIILRKRQG
                     SRGAMGHYVLAERE"
BASE COUNT      702 a    606 c    660 g    759 t
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  Query Match             99.4%;  Score 271.4;  DB 9;  Length 2727;
  Best Local Similarity   99.6%;  Pred. No. 4.2e-76;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 15
AR117795
LOCUS       AR117795                 1440 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 11 from patent US 6140305.
ACCESSION   AR117795
VERSION     AR117795.1  GI:14098701
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1440)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 11 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .1440
                     /organism="unknown"
BASE COUNT      347 a    354 c    408 g    331 t
ORIGIN

  Query Match             98.8%;  Score 269.8;  DB 6;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.3e-75;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Search completed: February 11, 2004, 19:15:40
Job time : 1636.78 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 15:39:52 ; Search time 1556.87 Seconds
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Title: 09981606-1A_COPY_67_339
Perfect score: 273
Sequence: 1 cgcttgctgcgttcacactc.....aaaatcacaaccacagcaag 273

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
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21: em_gss_fun:*
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25: em_gss_rod:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	271.4	99.4	560	9	AU279987	AU279987 AU279987
	3	269.8	98.8	535	14	CB162561	CB162561 K-EST0223
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	5	180.2	66.0	523	10	BF080089	BF080089 230846 MA
	6	180.2	66.0	550	12	BI339179	BI339179 364041 MA
c	7	175.8	64.4	464	9	AA217236	AA217236 mu89b05.r
	8	175.8	64.4	481	10	BB851691	BB851691 BB851691
	9	175.8	64.4	489	10	BE994943	BE994943 UI-M-CG0p
	10	175.8	64.4	714	14	BY747346	BY747346 BY747346
	11	175.8	64.4	1719	11	AK088986	AK088986 Mus muscu
	12	175.8	64.4	1723	11	AK009581	AK009581 Mus muscu
	13	175.4	64.2	819	10	BG747345	BG747345 602704818
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	15	174.8	64.0	668	14	BY745026	BY745026 BY745026
	16	163.2	59.8	502	10	BB858165	BB858165 BB858165
	17	137.6	50.4	407	13	BY159932	BY159932 BY159932
	18	136	49.8	481	13	BQ561639	BQ561639 H4071E07-
	19	136	49.8	542	14	CA569584	CA569584 K0445A07-
	20	123.8	45.3	364	13	BY202250	BY202250 BY202250
	21	122.2	44.8	351	13	BY319883	BY319883 BY319883
	22	116.6	42.7	825	13	BU746849	BU746849 CH3#007_D
	23	113.4	41.5	871	13	BU746860	BU746860 CH3#007_F
	24	111.6	40.9	344	13	BY196171	BY196171 BY196171
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	26	103.4	37.9	346	13	BY210730	BY210730 BY210730
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	33	77.2	28.3	435	13	BY157603	BY157603 BY157603
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	38	53.2	19.5	757	13	BU940705	BU940705 AGENCOURT
	39	53.2	19.5	765	9	AU138140	AU138140 AU138140
	40	53.2	19.5	818	14	CB960984	CB960984 AGENCOURT
	41	53.2	19.5	868	9	AL550540	AL550540 AL550540
	42	53.2	19.5	904	14	CA454707	CA454707 AGENCOURT
	43	53.2	19.5	934	13	BQ924251	BQ924251 AGENCOURT
	44	52.4	19.2	793	9	AU132916	AU132916 AU132916
	45	52.4	19.2	886	14	CD244248	CD244248 AGENCOURT

ALIGNMENTS

RESULT 1
BM751283
LOCUS BM751283 544 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0027329 S9SNU601 Homo sapiens cDNA clone S9SNU601-12-G03 5', mRNA sequence.
ACCESSION BM751283
VERSION BM751283.1 GI:19080901
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 544)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 12 row: G column: 03
High quality sequence stop: 544.

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="S9SNU601-12-G03"
                     /sex="M"
                     /tissue_type="Ascites"
                     /cell_type="Epithelial"
                     /cell_line="SNU-601"
                     /lab_host="Top10F'"
                     /clone_lib="S9SNU601"
                     /note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI;
                     Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including SfiI
                     site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized with Superscript II using SfiI
                     oligo-dT primer. After first strand synthesis, RNA was
                     degraded by NaOH treatment and cDNA was amplified by PCR
                     reaction. The PCR products were digested with SfiI and
                     cloned into DraIII- digested pME18S-FL3 vector. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT      120 a    141 c    162 g    121 t
ORIGIN

  Query Match             99.4%;  Score 271.4;  DB 12;  Length 544;
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  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        108 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 167

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        168 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 227

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Db        228 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 287

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        348 TGGACTATTATGGAAAATCACAACCACAGCAAG 380


RESULT 2
AU279987
LOCUS       AU279987                560 bp    mRNA    linear   EST 10-FEB-2003
DEFINITION  AU279987 CHONS2 Homo sapiens cDNA clone CHONS2002538 5', mRNA
            sequence.
ACCESSION   AU279987
VERSION     AU279987.1  GI:28299214
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 560)
  AUTHORS   Imabayashi,H., Gojo,S., Kiyono,T., Sugiyama,T., Irie,R., Isogai,T.,
            Mori,T., Hata,J., Tomoya,Y. and Umezawa,A.
  TITLE     Redifferentiation of dedifferentiated chondrocytes and
            chondrogenesis of human bone marrow stromal cells via chondrosphere
            formation with an expression profiling by large-scale cDNA analysis
  JOURNAL   Unpublished
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA Project, Sugiyama,T.; Wakamatsu,A.; Irie,R.; Umezawa
            ,A.; Fukuma,M.; Kusakari,S.; Hata,J.; Ishii,S.; Yamamoto,J.; Isono
            ,Y.; Saito,K.; Nakamura,Y.; Masuho,Y.; Nagai,K.; Isogai,T.
            HRI human cDNA project; cDNA library construction & 5'-end one
            pass sequencing: Helix Research Institute.
FEATURES             Location/Qualifiers
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                     /clone="CHONS2002538"
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                     /note="Vector: pME18SFL3"
BASE COUNT      125 a    143 c    168 g    124 t
ORIGIN

  Query Match             99.4%;  Score 271.4;  DB 9;  Length 560;
  Best Local Similarity   99.6%;  Pred. No. 6.4e-75;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        102 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 161

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Db        162 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 221

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Db        282 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 341

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db        342 TGGACTATTATGGAAAATCACAACCACAGCAAG 374


RESULT 3
CB162561
LOCUS       CB162561                535 bp    mRNA    linear   EST 30-JAN-2003
DEFINITION  K-EST0223175 L17N670205n1 Homo sapiens cDNA clone
            L17N670205n1-27-D07 5', mRNA sequence.
ACCESSION   CB162561
VERSION     CB162561.1  GI:28148687
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
```

```
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 27  row: D  column: 07
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L17N670205n1-27-D07"
                     /sex="F"
                     /lab_host="Top10F'"
                     /clone_lib="L17N670205n1"
                     /note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
                     Site_2: NotI; The library was contributed by the Soares
                     laboratory and it was constructed as described by Bonaldo,
                     M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
                     6(9): 791-806. RNA was prepared from harvested cell
                     culture."
BASE COUNT      113 a    140 c    161 g    121 t
ORIGIN

  Query Match             98.8%;  Score 269.8;  DB 14;  Length 535;
  Best Local Similarity   99.3%;  Pred. No. 2e-74;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 153

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 213

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 273

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 333

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||| ||||||||||||||||
Db        334 TGGACTATTATGGAATATCACAACCACAGCAAG 366


RESULT 4
BF883952/c
LOCUS       BF883952                384 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  PM4-ET0209-151200-003-f07 ET0209 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF883952
VERSION     BF883952.1  GI:12274078
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM4&t2=PM4-ET0209-
            151200-003-f07&t3=2000-12-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 17
            High quality sequence stop: 384.
FEATURES             Location/Qualifiers
     source          1. .384
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="ET0209"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       92 a    112 c     87 g     93 t
ORIGIN

  Query Match             81.5%;  Score 222.4;  DB 10;  Length 384;
  Best Local Similarity   99.2%;  Pred. No. 1.8e-59;
  Matches  234;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         38 TGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATG 97
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATG 325

Qy         98 ACCAGCTGTTCGTGTTCTATGATCATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGG 157
              |||||||| |||||||||||||||||| ||||||||||||||||||||||||||||||
Db        324 ACCAGCTG-TCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGG 266

Qy        158 TTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGG 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 TTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGG 206

Qy        218 ATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAG 150


RESULT 5
BF080089
LOCUS       BF080089                523 bp    mRNA    linear   EST 18-OCT-2000
DEFINITION  230846 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BF080089
VERSION     BF080089.1  GI:10873919
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush
            ,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
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            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 48  row: E  column: 9
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .523
                      /organism="Sus scrofa"
                      /mol_type="mRNA"
                      /db_xref="taxon:9823"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /clone_lib="MARC 2PIG"
                      /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                      Library made from pooled tissue from testis, ovary,
                      endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      103 a    175 c    152 g     93 t
ORIGIN

  Query Match             66.0%;  Score 180.2;  DB 10;  Length 523;
  Best Local Similarity   78.8%;  Pred. No. 5e-46;
  Matches  215;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||   || |||  ||||||| |||| || ||||||||||| ||||| ||||  || ||
Db        169 CGAGCGCCGCGGCCACACTCCCTGCTCTTCCTCTTCATGGGCGCCTCGGAGCCAGATCTC 228

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              || ||  || ||||||| || |||||||||||||| |||||||||| |||| |||  ||
Db        229 GGGCTGCCCCTGTTTGAGGCCTTGGGCTACGTGGACGACCAGCTGTTTGTGTCCTACAAT 288

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              || ||| |||||||||  ||||| ||  | || ||| | ||  |||      || | |||
Db        289 CACGAGAGTCGCCGTGCAGAGCCTCGCGCCCCCTGGCTCTCGGGTAAGGCCTCCAACCAA 348

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              |||||||||||||  || ||||| |||||||||||||||||||||||||| || ||||||
Db        349 CTGTGGCTGCAGCTAAGCCAGAGCCTGAAAGGGTGGGATCACATGTTCACCGTGGACTTC 408

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||| || ||||| || |||||| ||||||||
Db        409 TGGACCATCATGGACAACCACAACTACAGCAAG 441


RESULT 6
BI339179
LOCUS       BI339179                 550 bp    mRNA    linear   EST 30-JUL-2001
DEFINITION  364041 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI339179
VERSION     BI339179.1  GI:15032462
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush
            ,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
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            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 100  row: C  column: 24
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .550
                      /organism="Sus scrofa"
                      /mol_type="mRNA"
                      /db_xref="taxon:9823"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /clone_lib="MARC 2PIG"
                      /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                      Library made from pooled tissue from testis, ovary,
                      endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      108 a    180 c    164 g     98 t
ORIGIN

  Query Match             66.0%;  Score 180.2;  DB 12;  Length 550;
  Best Local Similarity   78.8%;  Pred. No. 5.2e-46;
  Matches  215;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||   || |||  ||||||| |||| || ||||||||||| ||||| ||||  || ||
Db        142 CGAGCGCCGCGGCCACACTCCCTGCTCTTCCTCTTCATGGGCGCCTCGGAGCCAGATCTC 201

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              || ||  || ||||||| || |||||||||||||| |||||||||| |||| |||  ||
Db        202 GGGCTGCCCCTGTTTGAGGCCTTGGGCTACGTGGACGACCAGCTGTTTGTGTCCTACAAT 261

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              || ||| |||||||||  ||||| ||  | || ||| | ||  |||      || | |||
Db        262 CACGAGAGTCGCCGTGCAGAGCCTCGCGCCCCCTGGCTCTCGGGTAAGGCCTCCAACCAA 321

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              |||||||||||||  || ||||| |||||||||||||||||||||||||| || ||||||
Db        322 CTGTGGCTGCAGCTAAGCCAGAGCCTGAAAGGGTGGGATCACATGTTCACCGTGGACTTC 381

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||| || ||||| || |||||| ||||||||
Db        382 TGGACCATCATGGACAACCACAACTACAGCAAG 414


RESULT 7
AA217236/c
LOCUS       AA217236                 464 bp    mRNA    linear   EST 06-FEB-1997
DEFINITION  mu89b05.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
            IMAGE:652689 5' similar to TR:G940354 G940354 CLASS I
            HISTOCOMPATIBILITY ANTIGEN-LIKE PROTEIN. ;, mRNA sequence.
ACCESSION   AA217236
VERSION     AA217236.1  GI:1826237
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 464)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
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            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:398537
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES              Location/Qualifiers
     source           1. .464
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:652689"
                      /sex="male"
                      /tissue_type="lymph node"
                      /dev_stage="4 weeks"
                      /lab_host="DH10B"
                      /clone_lib="Soares mouse lymph node NbMLN"
                      /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
                      with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      1st strand cDNA was primed with a Not I - oligo(dT) primer
                      [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGATACTTTTTTTTTTTTTTTTTTTTTTT
                      3']; double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. RNA
                      provided by Dr. Bertrand Jordan. Library constructed and
                      normalized by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      101 a    136 c    119 g    108 t
ORIGIN

  Query Match             64.4%;  Score 175.8;  DB 9;  Length 464;
  Best Local Similarity   78.7%;  Pred. No. 1.2e-44;
  Matches  210;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          7 CTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT 66
              | ||||||||| |||||    |||||||||||||||||||||||||  ||||| || ||
Db        453 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 394

Qy         67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
              | ||||||||| |||  |||||| ||||||||||||||| || |||| |||  ||||||||
Db        393 CCTTTGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG 334

Qy        127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG 186
              |||||||||  |||||| |  | || ||| | |       ||  |||||||| |||||
Db        333 AGTCGCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGG 274

Qy        187 CTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACT 246
              ||||| |||||||||||| ||||||||||||||  |||||||||  || ||||||||||
Db        273 CTGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 214

Qy        247 ATTATGGAAAATCACAACCACAGCAAG 273
              || ||||  ||  | ||||||| |||
Db        213 ATCATGGGCAACTATAACCACAGTAAG 187


RESULT 8
BB851691
LOCUS       BB851691                481 bp    mRNA    linear   EST 26-NOV-2001
DEFINITION  BB851691 RIKEN full-length enriched, B16 F10Y cells Mus musculus
            cDNA clone G370002P09 5', mRNA sequence.
ACCESSION   BB851691
VERSION     BB851691.1  GI:17093145
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 481)
  AUTHORS   Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
            Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
            ,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
            , Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
            ,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.
            , Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
            2001)
  JOURNAL   Unpublished
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES              Location/Qualifiers
     source           1. .481
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="G370002P09"
                      /cell_type="B16 F10Y cells"
                      /clone_lib="RIKEN full-length enriched, B16 F10Y cells"
BASE COUNT      95 a    134 c    140 g    112 t
ORIGIN

  Query Match             64.4%;  Score 175.8;  DB 10;  Length 481;
  Best Local Similarity   78.7%;  Pred. No. 1.2e-44;
  Matches  210;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          7 CTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT 66
              | ||||||||| |||||    |||||||||||||||||||||||||  ||||| || ||
Db        182 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 241

Qy         67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
              | ||||||||| |||  |||||| ||||||||||||||| || |||| |||  ||||||||
Db        242 CCTTTGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG 301

Qy        127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG 186
              |||||||||  |||||| |  | || ||| | |       ||  |||||||| |||||
Db        302 AGTCGCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGG 361

Qy        187 CTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACT 246
              ||||| |||||||||||| ||||||||||||||  |||||||||  || ||||||||||
Db        362 CTGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 421

Qy        247 ATTATGGAAAATCACAACCACAGCAAG 273
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                 || ||||  ||  | ||||||||| |||
Db        422 ATCATGGGCAACTATAACCACAGTAAG 448


RESULT 9
BE994943
LOCUS       BE994943                489 bp    mRNA    linear   EST 29-APR-2002
DEFINITION  UI-M-CG0p-bik-d-03-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
            UI-M-CG0p-bik-d-03-0-UI 3', mRNA sequence.
ACCESSION   BE994943
VERSION     BE994943.1  GI:10678689
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
            clones from RESEARCH GENETICS. It should be noted that Bento Soares
            is generating a small number of additional specialized
            non-redundant arrays of BMAP cDNAs whose availability will be
            considered under appropriate and limited collaborative arrangements
            The tissue for this library was contributed by Dr. Xin-Yuan Fu,
            Yale University School of Medicine The following repetitive
            elements were found in this cDNA sequence: 1-31, >(CAG
            )n#Simple_repeat
            Seq primer: M13 Forward
            POLYA=No.
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                     /clone="UI-M-CG0p-bik-d-03-0-UI"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NIH_BMAP_Ret4_S2"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_Ret4_S2 library is a subtracted library,
                     ultimately derived from mouse retina tissue libraries at
                     various stages of development. For a detailed description
                     of the library from which this clone was derived, please
                     visit our web site at brainest.eng.uiowa.edu. The tissue
                     for this library was contributed by Dr. Xin-Yuan Fu, Yale
                     University School of Medicine
                     TAG_SEQ=None found"
BASE COUNT      103 a    133 c    144 g    109 t
ORIGIN

  Query Match             64.4%;  Score 175.8;  DB 10;  Length 489;
  Best Local Similarity   78.7%;  Pred. No. 1.2e-44;
  Matches  210;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          7 CTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT 66
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Db         59 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 118

Qy         67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
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Db        119 CCTTTGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG 178

Qy        127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG 186
              |||||||||  |||||| |  | || ||| | |        ||  |||||||| |||||
Db        179 AGTCGCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGG 238

Qy        187 CTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACT 246
              ||||| |||||||||||| |||||||||||||  |||||||||  || ||||||||||
Db        239 CTGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 298

Qy        247 ATTATGGAAAATCACAACCACAGCAAG 273
              || ||||  ||  | |||||||| |||
Db        299 ATCATGGGCAACTATAACCACAGTAAG 325


RESULT 10
BY747346
LOCUS       BY747346                714 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY747346 RIKEN full-length enriched, 2 days neonate thymus thymic
            cells (NOD) Mus musculus cDNA clone E430034J19 5', mRNA sequence.
ACCESSION   BY747346
VERSION     BY747346.1  GI:27175512
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 714)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.
            , Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
            Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
            Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
            Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
            ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
            ,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.
            , Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
            Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
            King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
            ,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki
            ,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
            Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
            Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring
            ,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou
            ,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale
            ,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y.,
            Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa
            ,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
            Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura
            ,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.
            , Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii
            ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
            ,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
            ,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
            ,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
            Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
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          ,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
          Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
          Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
          Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
          Submission
           Computational Analysis of Full-Length Mouse cDNAs Compared with
          Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
           Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new
          genes. Genome Res. 10 (10), 1617-1630 (2000)
           RIKEN integrated sequence analysis (RISA) system--384-format
          sequencing pipeline with 384 multicapillary sequencer. Genome Res.
          10 (11), 1757-1771 (2000)
           Computer-based methods for the mouse full-length cDNA
          encyclopedia: real-time sequence clustering for construction of a
          nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
           cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
           Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
          Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
          Trust/MRC building Addenbrookes Hospital Cambridge) whose
          assistance we gratefully acknowledge.
           Please visit our web site (http://genome.gsc.riken.go.jp) for
          further details.
FEATURES             Location/Qualifiers
     source          1. .714
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="NOD"
                     /db_xref="taxon:10090"
                     /clone="E430034J19"
                     /tissue_type="thymus"
                     /cell_type="thymic cells"
                     /clone_lib="RIKEN full-length enriched, 2 days neonate
                     thymus thymic cells (NOD)"
BASE COUNT      166 a    194 c    208 g    146 t
ORIGIN

  Query Match           64.4%;  Score 175.8;  DB 14;  Length 714;
  Best Local Similarity   78.7%;  Pred. No. 1.5e-44;
  Matches  210;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          7 CTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT 66
              | ||||||||| |||||    ||||||||||||||||||||||||||  ||||| || ||
Db        178 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 237

Qy         67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
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Db        238 CCTTTGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG 297

Qy        127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG 186
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Db        298 AGTCGCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGG 357

Qy        187 CTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACT 246
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Db        358 CTGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 417

Qy        247 ATTATGGAAAATCACAACCACAGCAAG 273
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Db        418 ATCATGGGCAACTATAACCACAGTAAG 444


RESULT 11
AK088986
LOCUS       AK088986               1719 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN
            full-length enriched library, clone:E430034J19
            product:hemochromatosis, full insert sequence.
ACCESSION   AK088986
VERSION     AK088986.1  GI:26354115
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1719)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
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            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
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                     /note="putative"
     polyA_site      1719
                     /note="putative"
BASE COUNT      405 a    452 c    455 g    407 t
ORIGIN

  Query Match             64.4%;  Score 175.8;  DB 11;  Length 1719;
  Best Local Similarity   78.7%;  Pred. No. 2.2e-44;
  Matches  210;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          7 CTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT 66
              | ||||||||| |||||    |||||||||||||||||||||||||  ||||| || ||
Db        178 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 237

Qy         67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
               | |||||||| |||  |||||| |||||||||||||| || |||| |||  ||||||||
Db        238 CCTTTGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG 297

Qy        127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG 186
              |||||||||  ||||||  |   | || ||| | |        ||  ||||||||| |||||
Db        298 AGTCGCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGG 357

Qy        187 CTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACT 246
              |||||  |||||||||||  ||||||||||||||  |||||||||  || ||||||||||
Db        358 CTGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 417

Qy        247 ATTATGGAAAATCACAACCACAGCAAG 273
              || ||||  ||  | ||||||| |||
Db        418 ATCATGGGCAACTATAACCACAGTAAG 444


RESULT 12
AK009581
LOCUS       AK009581                1723 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
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            sequence.
ACCESSION   AK009581
VERSION     AK009581.1  GI:12844462
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
```

```
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1723)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES             Location/Qualifiers
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                     /sex="male"
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                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             99. .1178
                     /note="unnamed protein product; hemochromatosis
                     (MGD|MGI:109191)
                     putative"
                     /codon_start=1
                     /protein_id="BAB26373.1"
                     /db_xref="GI:12844463"
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                     CPKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLELGRGVLGQQV
                     PTLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVLPNGDETY
                     QGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVG
                     ILFLILRKRKASGGTMGGYVLTDCE"
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                     /note="putative"
     polyA_site      1723
                     /note="putative"
BASE COUNT      406 a    456 c    454 g    407 t
ORIGIN

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  Best Local Similarity   78.7%;  Pred. No. 2.3e-44;
  Matches  210;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          7 CTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT 66
              | |||||||| ||||     ||||||||||||||||||||||||| |||| || ||
Db        183 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 242

Qy         67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
               | |||||||| |||  |||||| ||||||||||||| || |||| |||  ||||||||
Db        243 CCTTTGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG 302

Qy        127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG 186
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Db        303 AGTCGCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGG 362

Qy        187 CTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACT 246
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Db        363 CTGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 422

Qy        247 ATTATGGAAAATCACAACCACAGCAAG 273
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Db        423 ATCATGGGCAACTATAACCACAGTAAG 449


RESULT 13
BG747345
LOCUS       BG747345                819 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602704818F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857941 5',
            mRNA sequence.
ACCESSION   BG747345
VERSION     BG747345.1  GI:14057998
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1711  row: d  column: 06
            High quality sequence stop: 792.
FEATURES             Location/Qualifiers
     source          1. .819
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4857941"
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                     /clone_lib="NIH_MGC_15"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT      202 a    201 c    235 g    181 t
ORIGIN
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  Query Match             64.2%;  Score 175.4;  DB 10;  Length 819;
  Best Local Similarity   99.4%;  Pred. No. 2.1e-44;
  Matches  176;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          97 GACCAGCTGTTCGTGTTCTATGATCATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGG 156
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Db          61 GTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGG 120

Qy         217 GATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Db         121 GATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAG 177


RESULT 14
BF465475
LOCUS       BF465475                392 bp    mRNA    linear   EST 04-DEC-2000
DEFINITION  UI-M-CG0p-bqp-a-01-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
            UI-M-CG0p-bqp-a-01-0-UI 3', mRNA sequence.
ACCESSION   BF465475
VERSION     BF465475.1  GI:11534658
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
            clones from RESEARCH GENETICS. It should be noted that Bento Soares
            is generating a small number of additional specialized
            non-redundant arrays of BMAP cDNAs whose availability will be
            considered under appropriate and limited collaborative arrangements
            The following repetitive elements were found in this cDNA sequence:
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
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                     /clone_lib="NIH_BMAP_Ret4_S2"
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                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_Ret4_S2 library is a subtracted library,
                     ultimately derived from mouse retina tissue libraries at
                     various stages of development. For a detailed description
                     of the library from which this clone was derived, please
                     visit our web site at brainest.eng.uiowa.edu. The tissue
                     for this library was contributed by Dr. Xin-Yuan Fu, Yale
                     University School of Medicine
                     TAG_SEQ=None found"
BASE COUNT       74 a    107 c    115 g     93 t      3 others
ORIGIN

  Query Match             64.0%;  Score 174.8;  DB 10;  Length 392;
  Best Local Similarity   78.3%;  Pred. No. 2.3e-44;
  Matches  209;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy           7 CTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT 66
               | ||||||||| |||||    ||||||||||||||||||||||||  ||||| || ||
Db          59 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 118

Qy          67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
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Db         179 AGTCGCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGG 238

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RESULT 15
BY745026
LOCUS       BY745026                668 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY745026 RIKEN full-length enriched, bone marrow macrophage Mus
            musculus cDNA clone I830071K08 5', mRNA sequence.
ACCESSION   BY745026
VERSION     BY745026.1  GI:27171997
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 668)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.
            , Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
            Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
            Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
            Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
            ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
            ,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.
            , Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
            Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
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            Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring
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            ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
            ,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
            ,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
```

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda ,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno ,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .668
/organism="Mus musculus"
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/clone="I830071K08"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"

BASE COUNT 138 a 177 c 200 g 148 t 5 others
ORIGIN

Query Match 64.0%; Score 174.8; DB 14; Length 668;
Best Local Similarity 78.3%; Pred. No. 2.9e-44;
Matches 209; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Qy          7 CTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT 66
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Db        200 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 259

Qy         67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
               | ||||||||| |||  |||||| ||||||||||||||| || |||| |||  ||||||||
Db        260 CCTTTGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG 319

Qy        127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG 186
              |||||||||  ||||||  |   | || ||| | |         |  |||||||| |||||
Db        320 AGTCGCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCANACCTCAAGCCAGCTGTGG 379

Qy        187 CTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACT 246
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OM nucleic - nucleic search, using sw model

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(without alignments)
3668.467 Million cell updates/sec

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Perfect score: 273
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	271.4	99.4	1317	24	ABK49917	DNA encoding beta
2	271.4	99.4	1440	18	AAT96691	Hereditary haemoch
3	271.4	99.4	1440	22	AAC68429	Human hereditary h
4	271.4	99.4	1440	22	AAC68430	Human hereditary h
5	271.4	99.4	2506	21	AAA96769	cDNA sequence enco
6	271.4	99.4	2727	19	AAV23525	Haemochromatosis g
7	269.8	98.8	1440	22	AAC68431	Human hereditary h
8	269.8	98.8	1440	22	AAC68432	Human hereditary h
9	261.4	95.8	5982	25	ABV93934	Human colon specif
10	261.4	95.8	10825	18	AAT96690	Hereditary haemoch
11	261.4	95.8	10825	22	AAC68425	Human hereditary h
12	261.4	95.8	10825	22	AAC68426	Human hereditary h
13	261.4	95.8	12146	21	AAA96794	Genomic DNA of a h
c 14	261.4	95.8	235033	19	AAV57926	Hereditary haemoch
c 15	261.4	95.8	237326	19	AAV57903	Hereditary haemoch
16	259.8	95.2	10825	22	AAC68427	Human hereditary h
17	259.8	95.2	10825	22	AAC68428	Human hereditary h
18	259	94.9	596	22	AAI63897	Human polynucleoti
19	98.4	36.0	100	22	AAH02413	Human HLA-H exon 2
20	96.8	35.5	100	22	AAH02414	Human HLA-H exon 2
c 21	74.4	27.3	76	22	AAF58231	Oligonucleotide D1
c 22	72.8	26.7	76	22	AAF58232	Oligonucleotide D1
c 23	68.4	25.1	75	22	AAF58246	Oligonucleotide D1
c 24	66.8	24.5	75	22	AAF58247	Oligonucleotide D1
25	54.4	19.9	575	22	AAI63896	Human polynucleoti
26	53.2	19.5	491	21	AAC01392	Human secreted pro
27	51	18.7	51	21	AAA62424	Human HFE peptide
28	48.2	17.7	430	22	AAF92308	Bovine mammary tis
29	45.4	16.6	47	22	AAH78015	DNA fragment with
30	45	16.5	45	21	AAA12669	Probe used for gen
31	43.8	16.0	1112	21	AAA48668	cDNA encoding chic
32	43.6	16.0	1032	20	AAX89246	MHC class I antige
33	42	15.4	1032	20	AAX89245	MHC class I antige
34	41.6	15.2	2380	19	AAV34456	Human MHC class I
35	40.6	14.9	264	24	AAD29183	Chicken MHc class
36	40.6	14.9	3324	20	AAX60262	Nucleic acid seque
37	40	14.7	448	22	AAI63914	Human polynucleoti
38	40	14.7	1001	22	AAI63816	Human polynucleoti
39	40	14.7	12930	25	ABZ74995	Human MHC class I
40	39.6	14.5	261	24	ABK88254	YF-VI DNA sequence
41	39.6	14.5	261	24	AAD29186	Chicken MHc class
42	38.8	14.2	313	21	AAC08552	Human secreted pro
43	38.4	14.1	40	22	AAC68459	Sequence surroundi
44	38.4	14.1	148834	24	ABK83570	Human cDNA differe
45	37.8	13.8	1230	21	AAA48669	cDNA encoding chic

ALIGNMENTS

RESULT 1
ABK49917
ID ABK49917 standard; cDNA; 1317 BP.
XX
AC ABK49917;
XX
DT 15-JUL-2002 (first entry)
XX
DE DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
XX
KW Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
KW iron absorption regulator; intracellular iron absorption; lung injury;
KW haemochromatosis; transfusion; thalassaemia; haemolytic anaemia;
KW chronic infection; transferrin receptor; TfR; brain tumour; cancer;
KW oxidative stress disorder; tissue damage; vascular disease;
KW inflammation; atherosclerosis; autoimmune disease;
KW inflammatory condition; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1317
FT /*tag= a
FT /product= "beta2M/HFE monochain"
XX
PN WO200224929-A2.
XX
PD 28-MAR-2002.
XX
PF 24-SEP-2001; 2001WO-US29873.
XX

```
PR   22-SEP-2000; 2000US-234843P.
XX
PA   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA   (MCIN/) MCINNIS P.
XX
PI   Ehrlich R,  Rotem-Yehudar R,  Laham N;
XX
DR   WPI; 2002-383192/41.
DR   P-PSDB; AAU80035.
XX
PT   Soluble beta 2 microglobulin/HFE monochain useful for treating
PT   iron-overload conditions e.g. thalassemia and chronic infections,
PT   comprises human beta 2 microglobulin linked to alpha domains of HFE by
PT   a linker peptide  -
XX
PS   Example 2; Fig 2; 77pp; English.
XX
CC   The invention relates to a soluble polypeptide (I) of beta 2
CC   microglobulin (beta2m)/HFE monochain comprising human beta2m (or its
CC   analogue or active fragment), linked to alpha1-alpha3 domains of human
CC   HFE (a central regulator of iron absorption; undefined), or its analogue
CC   or active fragment, by a flexible linker peptide, or a functional
CC   derivative or salt of (I). (I) is useful for reducing intracellular iron
CC   absorption in patients having hereditary haemochromatosis, transfusions,
CC   thalassaemias, haemolytic anaemia or chronic infections, and for
CC   delivering a therapeutic to cells that over-express transferrin receptor
CC   (TfR) which are preferably lymphocytes or leukocytes, across the blood-
CC   brain barrier. (I) is further useful for treating brain tumour. (I)
CC   is also useful for treating oxidative stress disorders resulting in
CC   tissue damage e.g. vascular diseases, inflammation, atherosclerosis,
CC   lung injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful
CC   as a platform for drug delivery of therapeutic use for cancer,
CC   autoimmune diseases and inflammatory conditions. The monochain manifests
CC   specific characteristics advantageous for drug delivery systems. It is a
CC   soluble, stable and fully conformed protein. It binds specifically to
CC   transferrin receptor (TfR) and therefore targets cells that over-express
CC   this receptor. It is continuously internalised by the target cells, thus
CC   enabling efficient drug delivery. It dissociates from the receptor in the
CC   cells, minimising side effects. It negatively regulates iron absorption,
CC   reducing growth of undesired cells and preventing lymphocyte activation.
CC   It is not diluted in the blood as is transferrin. It should not induce an
CC   immune response since it is a self non-polymeric protein and delivery of
CC   drugs via monochain is expected to overcome drug-resistance since it is a
CC   natural TfR-binding protein. The present sequence represents the
CC   coding sequence of beta2m/HFE monochain.
XX
SQ   Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;

  Query Match           99.4%;  Score 271.4;  DB 24;  Length 1317;
  Best Local Similarity   99.6%;  Pred. No. 2.7e-79;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        403 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 462

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 522

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 582

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 642

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        643 TGGACTATTATGGAAAATCACAACCACAGCAAG 675
```

```
RESULT 2
AAT96691
ID   AAT96691 standard; cDNA; 1440 BP.
XX
AC   AAT96691;
XX
DT   14-APR-1998  (first entry)
XX
DE   Hereditary haemochromatosis gene cDNA clone.
XX
KW   Hereditary haemochromatosis; metal toxicity; diagnosis;
KW   gene therapy; prenatal screening; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             222.1268
FT                   /*tag=  a
FT   mutation        408
FT                   /*tag=  g
FT                   /note= "C to G substitution (24d2 mutation)
FT                          results in His to Asp substitution"
FT   variation       414
FT                   /*tag=  h
FT                   /note= "A to T substitution (24d7 variant)
FT                          results in Ser to Cys substitution"
FT   mutation        1066
FT                   /*tag=  i
FT                   /note= "G to A substitution (24d1 mutation
FT                          associated with HH), results in Cys to
FT                          Tyr substitution"
XX
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US06254.
XX
PR   23-MAY-1996;   96US-0652265.
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   P-PSDB; AAW36499.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis
PT   and treatment of hereditary haemochromatosis disease
XX
PS   Disclosure; Fig 4; 115pp; English.
XX
CC   This cDNA clone, designated cDNA24, is derived from human gene
CC   whose mutated form is associated with hereditary haemochromatosis
CC   (HH).  It was obtained from a directionally cloned plasmid-based
CC   cDNA library following identification of the HH locus in the HLA
CC   region of chromosome 6.  A single mutation (24d1) in the HH gene
CC   appears responsible for the majority of HH disease.  This comprises
CC   a G to A substitution that is present in 86% of affected
CC   chromosomes and in 4% of unaffected chromosomes.  It results in a
CC   Cys to Tyr substitution in the encoded protein (see AAW36499) at a
CC   critical disulphide bridge important for secondary structure.  The
CC   following are claimed: a 10825 bp genomic DNA sequence (I) (see
CC   AAT96690), the 1437 bp cDNA sequence (Ia) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a
CC   peptide product chosen from the HH gene product, its variants
CC   (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC   residues of these; an antibody produced using the peptide; a method
CC   to determine the presence or absence of the common HH gene
CC   mutation; an animal model for the HH disease; metal chelation
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CC   agents, T-cell differentiation factors and therapeutic agents for
CC   the mitigation of injury due to oxidative process in vivo or
CC   mitigation of iron overload; a method for screening potential
CC   therapeutic agents for activity in connection with HH disease; an
CC   antisense oligonucleotide directed against a transcriptional
CC   product of a nucleic acid sequence as above; and oligonucleotides
CC   or pairs of oligonucleotides covering a range of nucleotides from
CC   (I), (Ia) or their variants, useful for detecting a polymorphism in
CC   the HH gene.  The invention also relates to methods for screening
CC   for HH homozygotes, to HH diagnosis, prenatal screening and
CC   diagnosis, and therapies of HH disease, including gene therapy,
CC   protein- and antibody-based therapeutics, and small molecule
CC   therapeutics.
XX
SQ   Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

  Query Match             99.4%;  Score 271.4;  DB 18;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 2.8e-79;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 3
AAC68429
ID   AAC68429 standard; DNA; 1440 BP.
XX
AC   AAC68429;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

  Query Match             99.4%;  Score 271.4;  DB 22;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 2.8e-79;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 4
AAC68430
ID   AAC68430 standard; DNA; 1440 BP.
XX
AC   AAC68430;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d1 mutation cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
```

```
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;

  Query Match             99.4%;  Score 271.4;  DB 22;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 2.8e-79;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 5
AAA96769
ID   AAA96769 standard; cDNA; 2506 BP.
XX
AC   AAA96769;
XX
DT   19-FEB-2001  (first entry)
XX
DE   cDNA sequence encoding a histocompatibility iron loading (HFE) protein.
XX
KW   Human; histocompatibility iron loading protein; HFE protein;
KW   major histocompatibility complex; non-classical class I gene;
KW   chromosome 6p; iron disorder; haemochromatosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1044
FT                   /*tag=  a
FT                   /product= "histocompatibility iron loading (HFE) protein"
FT   sig_peptide     1..66
FT                   /*tag=  b
FT   mutation        187
FT                   /*tag=  c
FT                   /note= "if this base is mutated to G, then the
FT                          protein contains the mutation H63D"
FT   mutation        193
FT                   /*tag=  d
FT                   /note= "if this base is mutated to T, then the
FT                          protein contains the mutation S65C"
FT   mutation        277
FT                   /*tag=  e
FT                   /note= "if this base is mutated to C, then the
FT                          protein contains the mutation G93R"
FT   mutation        314
FT                   /*tag=  f
FT                   /note= "if this base is mutated to C, then the
FT                          protein contains the mutation I105T, which
FT                          is associated with an iron overload disorder"
XX
PN   WO200058515-A1.
XX
PD   05-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US07982.
XX
PR   26-MAR-1999;   99US-0277457.
XX
PA   (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI   Rothenberg BE,  Sawada-Hirai R,  Barton JC;
XX
DR   WPI; 2000-647244/62.
DR   P-PSDB; AAB19149.
XX
PT   Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT   susceptibility to develop it, by determining the presence of a mutation
PT   in exon 2 or an intron of a histocompatibility iron loading nucleic
PT   acid -
XX
PS   Disclosure; Page 2-3; 55pp; English.
XX
CC   The present sequence encodes a human histocompatibility iron loading
CC   (HFE) protein. The HFE gene is a major histocompatibility (MHC)
CC   non-classical class I gene located on chromosome 6p. Mutations in the
CC   gene lead to iron disorders. The specification describes a method for
CC   diagnosing an iron disorder or a genetic susceptibility to develop the
CC   disorder in a mammal. The method comprises determining the presence of
CC   a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
CC   is not a C to G missense mutation at nucleotide 187 of the sequence
CC   given in A96769 (Genbank Accession number U60319). The presence of the
CC   mutation indicates the disorder or the genetic susceptibility to the
CC   disorder. The method is used to diagnose an iron disorder
CC   e.g. haemochromatosis, or a genetic susceptibility to develop it.
XX
SQ   Sequence 2506 BP; 648 A; 552 C; 596 G; 710 T; 0 other;

  Query Match             99.4%;  Score 271.4;  DB 21;  Length 2506;
  Best Local Similarity   99.6%;  Pred. No. 3.5e-79;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 126

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 186

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 246

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 306

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        307 TGGACTATTATGGAAAATCACAACCACAGCAAG 339


RESULT 6
AAV23525
ID   AAV23525 standard; mRNA; 2727 BP.
XX
AC   AAV23525;
```

```
XX
DT   10-JUL-1998  (first entry)
XX
DE   Haemochromatosis gene.
XX
KW   Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
KW   autosomal recessive disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO9807884-A1.
XX
PD   26-FEB-1998.
XX
PF   22-AUG-1997;   97WO-AU00539.
XX
PR   03-SEP-1996;   96AU-0002083.
PR   23-AUG-1996;   96AU-0001849.
XX
PA   (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI   Busfield F,  Cullen LM,  Jazwinska EC,  Powell LW;
XX
DR   WPI; 1998-179064/16.
XX
PT   Detection of autosomal recessive disorder - particularly hereditary
PT   haemochromatosis, by detecting a mutation in the HC gene
XX
PS   Disclosure; Page -; 32pp; English.
XX
CC   This sequence represents the haemochromatosis (HC) gene. Mutations in
CC   this sequence are detected using the method of the invention. The method
CC   is for identifying an individual with hereditary haemochromatosis (HH) or
CC   a predisposition to develop HH or to genetically pass on HH to an
CC   offspring, comprising isolating a biological sample and amplifying a
CC   region of genomic DNA in the biological sample encompassing all or part
CC   of the DNA between markers D6S265 and D6S276, and detecting at least one
CC   homozygous or heterozygous mutation in a nucleotide within the region.
CC   The method can also be used for identifying an individual with an
CC   autosomal recessive disorder (ARD) or predisposition to develop and/or
CC   genetically pass on an ARD to an offspring, comprises isolating a
CC   biological sample from the individual and screening genomic DNA in the
CC   sample for the presence of a homozygous or heterozygous mutation in a
CC   gene, the normal function of which, is required to prevent progression of
CC   the disorder. The method(s) can be used to identify individuals that are
CC   homozygous or heterozygous (carriers) for the mutation causing the ARD.
CC   Especially the method is used to diagnose HH or predisposition to HH by
CC   detecting a Cys282Tyr substitution. Individuals homozygous for this
CC   mutation have HH and heterozygotes are potential carriers of the
CC   disease.
XX
SQ   Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;

  Query Match             99.4%;  Score 271.4;  DB 19;  Length 2727;
  Best Local Similarity   99.6%;  Pred. No. 3.6e-79;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 7
AAC68431
ID   AAC68431 standard; DNA; 1440 BP.
XX
AC   AAC68431;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d2 mutation cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 347 A; 354 C; 408 G; 331 T; 0 other;

  Query Match             98.8%;  Score 269.8;  DB 22;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 9.3e-79;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
```

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                ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 8
AAC68432
ID   AAC68432 standard; DNA; 1440 BP.
XX
AC   AAC68432;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d1/2 mutation cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 348 A; 354 C; 407 G; 331 T; 0 other;

  Query Match             98.8%;  Score 269.8;  DB 22;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 9.3e-79;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 9
ABV93934
ID   ABV93934 standard; DNA; 5982 BP.
XX
AC   ABV93934;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Human colon specific nucleic acid, SEQ ID 25.
XX
KW   Human; colon; cytostatic; vaccine; gene therapy; colon cancer;
KW   colon disorder; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200277234-A2.
XX
PD   03-OCT-2002.
XX
PF   31-OCT-2001; 2001WO-US48414.
XX
PR   31-OCT-2000; 2000US-244758P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Sun Y,  Recipon H,  Ghosh MG,  Liu C;
XX
DR   WPI; 2003-018928/01.
XX
PT   New isolated colon-specific nucleic acid molecule, useful for treating
PT   colon cancer, and diagnosing or monitoring the presence of metastases
PT   of colon cancer in a patient  -
XX
PS   Claim 1; Page 155-156; 216pp; English.
XX
CC   The present invention relates to human colon specific nucleic acids
CC   (ABV93910-ABV94009) and proteins (ABP68360-ABP68435). The nucleic acids
CC   and proteins are useful for treating colon cancer and colon disorders,
CC   and diagnosing or monitoring the presence of colon disorders and
CC   metastases of colon cancer in a patient.
XX
SQ   Sequence 5982 BP; 1659 A; 1247 C; 1518 G; 1556 T; 2 other;

  Query Match             95.8%;  Score 261.4;  DB 25;  Length 5982;
  Best Local Similarity   99.6%;  Pred. No. 1e-75;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3402 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3461

Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       3462 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3521

Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3522 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3581

Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3582 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 3641

Qy        251 TGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||
Db       3642 TGGAAAATCACAACCACAGCAAG 3664


RESULT 10
AAT96690
```

```
ID   AAT96690 standard; DNA; 10825 BP.
XX
AC   AAT96690;
XX
DT   14-APR-1998  (first entry)
XX
DE   Hereditary haemochromatosis gene.
XX
KW   Hereditary haemochromatosis; metal toxicity; diagnosis;
KW   gene therapy; prenatal screening; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             361..7147
FT                   /*tag= a
FT                   /note= "contains introns"
FT   intron          437..3761
FT                   /*tag= b
FT                   /number= 1
FT   intron          4026..4234
FT                   /*tag= c
FT                   /number= 2
FT   intron          4511..5605
FT                   /*tag= d
FT                   /number= 3
FT   intron          5882..6039
FT                   /*tag= e
FT                   /number= 4
FT   intron          6154..7106
FT                   /*tag= f
FT                   /number= 5
FT   mutation        3872
FT                   /*tag= g
FT                   /note= "C to G substitution (24d2 mutation)
FT                          results in His to Asp substitution"
FT   variation       3878
FT                   /*tag= h
FT                   /note= "A to T substitution (24d7 variant)
FT                          results in Ser to Cys substitution"
FT   mutation        5834
FT                   /*tag= i
FT                   /note= "G to A substitution (24d1 mutation
FT                          associated with HH), results in Cys to
FT                          Tyr substitution"
FT
XX
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US06254.
XX
PR   23-MAY-1996;   96US-0652265.
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   P-PSDB; AAW36499.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis
PT   and treatment of hereditary haemochromatosis disease
XX
PS   Disclosure; Fig 3; 115pp; English.
XX
CC   This genomic DNA sequence corresponds to the human gene whose
CC   mutated form is associated with hereditary haemochromatosis (HH).
CC   To identify this novel gene, allelic association patterns were
CC   determined between known markers and the HH locus in the HLA region
CC   of chromosome 6.  A physical clone coverage was then generated
CC   extending from D6S265, which is a marker that is centromeric of
CC   HLA-A, in a telomeric direction through D6S276, a marker at which
CC   the allelic association was no longer observed.  A single mutation
CC   (24d1) in the HH gene appears responsible for the majority of HH
CC   disease.  This comprises a G to A substitution that is present in
CC   86% of affected chromosomes and in 4% of unaffected chromosomes.
CC   It results in a Cys to Tyr substitution in the encoded protein (see
CC   AAW36499) at a critical disulphide bridge important for secondary
CC   structure.  The following are claimed: the HH genomic DNA (I), a
CC   1437 bp cDNA sequence (Ia) (see AAT96691) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a
CC   peptide product chosen from the HH gene product, its variants
CC   (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC   residues of these; an antibody produced using the peptide; a method
CC   to determine the presence or absence of the common HH gene
CC   mutation; an animal model for the HH disease; metal chelation
CC   agents, T-cell differentiation factors and therapeutic agents for
CC   the mitigation of injury due to oxidative process in vivo or
CC   mitigation of iron overload; a method for screening potential
CC   therapeutic agents for activity in connection with HH disease; an
CC   antisense oligonucleotide directed against a transcriptional
CC   product of a nucleic acid sequence as above; and oligonucleotides
CC   or pairs of oligonucleotides covering a range of nucleotides from
CC   (I), (Ia) or their variants, useful for detecting a polymorphism in
CC   the HH gene.  The invention also relates to methods for screening
CC   for HH homozygotes, to HH diagnosis, prenatal screening and
CC   diagnosis, and therapies of HH disease, including gene therapy,
CC   protein- and antibody-based therapeutics, and small molecule
CC   therapeutics.
XX
SQ   Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;

  Query Match             95.8%;  Score 261.4;  DB 18;  Length 10825;
  Best Local Similarity   99.6%;  Pred. No. 1.3e-75;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy          71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy         131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy         191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy         251 TGGAAAATCACAACCACAGCAAG 273
               |||||||||||||||||||||||
Db        4002 TGGAAAATCACAACCACAGCAAG 4024


RESULT 11
AAC68425
ID   AAC68425 standard; DNA; 10825 BP.
XX
AC   AAC68425;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
OS   Homo sapiens.
XX
```

PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
DR P-PSDB; AAB36869.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;

Query Match 95.8%; Score 261.4; DB 22; Length 10825;
Best Local Similarity 99.6%; Pred. No. 1.3e-75;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        251 TGGAAAATCACAACCACAGCAAG 273
               |||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAG 4024
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RESULT 12
AAC68426
ID AAC68426 standard; DNA; 10825 BP.
XX
AC AAC68426;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis 24d1 mutation DNA.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ds.
XX
OS Homo sapiens.
XX

PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
DR P-PSDB; AAB36870.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;

Query Match 95.8%; Score 261.4; DB 22; Length 10825;
Best Local Similarity 99.6%; Pred. No. 1.3e-75;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
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Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
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Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Qy        251 TGGAAAATCACAACCACAGCAAG 273
               |||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAG 4024
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RESULT 13
AAA96794
ID AAA96794 standard; cDNA; 12146 BP.
XX
AC AAA96794;
XX
DT 19-FEB-2001 (first entry)
XX
DE Genomic DNA of a histocompatibility iron loading (HFE) gene.
XX
KW Human; histocompatibility iron loading protein; HFE protein;
KW major histocompatibility complex; non-classical class I gene;
KW chromosome 6p; iron disorder; haemochromatosis; ss.
XX
OS Homo sapiens.

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FT                   /*tag=  m
XX
PN   WO200058515-A1.
XX
PD   05-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US07982.
XX
PR   26-MAR-1999;   99US-0277457.
XX
PA   (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI   Rothenberg BE,  Sawada-Hirai R,  Barton JC;
XX
DR   WPI; 2000-647244/62.
XX
PT   Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT   susceptibility to develop it, by determining the presence of a mutation
PT   in exon 2 or an intron of a histocompatibility iron loading nucleic
PT   acid -
XX
PS   Example 1; Page 21-28; 55pp; English.
XX
CC   The present sequence represents the human histocompatibility iron
CC   loading (HFE) gene. The HFE gene is a major histocompatibility (MHC)
CC   non-classical class I gene located on chromosome 6p. Mutations in the
CC   gene lead to iron disorders. The specification describes a method for
CC   diagnosing an iron disorder or a genetic susceptibility to develop the
CC   disorder in a mammal. The method comprises determining the presence of
CC   a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
CC   is not a C to G missense mutation at nucleotide 187 of the sequence
CC   given in A96769 (Genbank Accession number U60319). The presence of the
CC   mutation indicates the disorder or the genetic susceptibility to the
CC   disorder. The method is used to diagnose an iron disorder
CC   e.g. haemochromatosis, or a genetic susceptibility to develop it.
XX
SQ   Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 other;

  Query Match             95.8%;  Score 261.4;  DB 21;  Length 12146;
  Best Local Similarity   99.6%;  Pred. No. 1.4e-75;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy          71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
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Db        4712 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 4771

Qy         131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Db        4772 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 4831

Qy         191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Qy         251 TGGAAAATCACAACCACAGCAAG 273
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Db        4892 TGGAAAATCACAACCACAGCAAG 4914


RESULT 14
AAV57926/c
ID   AAV57926 standard; DNA; 235033 BP.
XX
AC   AAV57926;
XX
DT   23-DEC-1998  (first entry)
XX
DE   Hereditary haemochromatosis subregion from an unaffected individual.
XX
KW   Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW   diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW   BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW   type 1 sodium transport gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO9814466-A1.
XX
PD   09-APR-1998.
XX
PF   30-SEP-1997;   97WO-US17658.
XX
PR   07-MAY-1997;   97US-0852495.
PR   01-OCT-1996;   96US-0724394.
XX
PA   (PROG-) PROGENTIOR INC.
XX
PI   Feder JN,  Kronmal GS,  Lauer PM,  Ruddy DA,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1998-240014/21.
XX
PT   Hereditary haemochromatosis gene products - used to develop products
PT   for the diagnosis and treatment of hereditary disorders in iron
PT   metabolism
XX
PS   Example 2; Fig 8; 209pp; English.
XX
CC   The present invention describes hereditary haemochromatosis gene
CC   products from the human haemochromatosis gene. The present sequence
CC   represents a hereditary haemochromatosis subregion from an individual
CC   unaffected by hereditary haemochromatosis (HH). Also described is a
CC   method to determine the presence or absence of the common hereditary
```

```
CC   haemochromatosis (HFE) gene mutation in an individual comprising:
CC   (a) providing DNA or RNA from the individual; and (b) assessing the
CC   DNA or RNA for the presence or absence of a haplotype or genotype where
CC   the presence or absence of the haplotype genotype indicates the likely
CC   presence of the HFE gene mutation in the genome of the individual. The
CC   HFE gene sequences from the present invention can be used to develop
CC   products for use in the diagnosis and treatment of HFE. The present
CC   invention also describes BTF genes, which are homologues of the milk
CC   protein butyrophilin (BT), and can be used in the production of agonists
CC   and antagonists of BT function. Also described are: (1) a RoRet gene
CC   which can be used to develop products for the study, diagnosis and
CC   treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC   which are homologues of a type 1 sodium transport gene, and can
CC   similarly be used for hypophosphatemia.
XX
SQ   Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;

  Query Match             95.8%;  Score 261.4;  DB 19;  Length 235033;
  Best Local Similarity   99.6%;  Pred. No. 4.8e-75;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
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Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Qy        251 TGGAAAATCACAACCACAGCAAG 273
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Db      43148 TGGAAAATCACAACCACAGCAAG 43126


RESULT 15
AAV57903/c
ID   AAV57903 standard; DNA; 237326 BP.
XX
AC   AAV57903;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Hereditary haemochromatosis subregion from an HH affected individual.
XX
KW   Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW   diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW   BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW   type 1 sodium transport gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO9814466-A1.
XX
PD   09-APR-1998.
XX
PF   30-SEP-1997;   97WO-US17658.
XX
PR   07-MAY-1997;   97US-0852495.
PR   01-OCT-1996;   96US-0724394.
XX
PA   (PROG-) PROGENTIOR INC.
XX
PI   Feder JN,  Kronmal GS,  Lauer PM,  Ruddy DA,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1998-240014/21.
XX
PT   Hereditary haemochromatosis gene products - used to develop products
PT   for the diagnosis and treatment of hereditary disorders in iron
PT   metabolism
XX
PS   Claim 1; Fig 9; 209pp; English.
XX
CC   The present invention describes hereditary haemochromatosis gene
CC   products from the human haemochromatosis gene. The present sequence
CC   represents a hereditary haemochromatosis subregion from an hereditary
CC   haemochromatosis (HH) affected individual. Also described is a
CC   method to determine the presence or absence of the common hereditary
CC   haemochromatosis (HFE) gene mutation in an individual comprising:
CC   (a) providing DNA or RNA from the individual; and (b) assessing the
CC   DNA or RNA for the presence or absence of a haplotype or genotype where
CC   the presence or absence of the haplotype genotype indicates the likely
CC   presence of the HFE gene mutation in the genome of the individual. The
CC   HFE gene sequences from the present invention can be used to develop
CC   products for use in the diagnosis and treatment of HFE. The present
CC   invention also describes BTF genes, which are homologues of the milk
CC   protein butyrophilin (BT), and can be used in the production of agonists
CC   and antagonists of BT function. Also described are: (1) a RoRet gene
CC   which can be used to develop products for the study, diagnosis and
CC   treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC   which are homologues of a type 1 sodium transport gene, and can
CC   similarly be used for hypophosphatemia.
XX
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  Query Match             95.8%;  Score 261.4;  DB 19;  Length 237326;
  Best Local Similarity   99.6%;  Pred. No. 4.9e-75;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
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Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Db      43158 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43099

Qy        251 TGGAAAATCACAACCACAGCAAG 273
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	273	100.0	1440	13	US-10-138-888-77	Sequence 77, Appl
	2	271.4	99.4	1440	13	US-10-138-888-9	Sequence 9, Appli
	3	271.4	99.4	1440	13	US-10-138-888-10	Sequence 10, Appl
	4	271.4	99.4	2506	13	US-09-981-606-1	Sequence 1, Appli
	5	269.8	98.8	1440	13	US-10-138-888-11	Sequence 11, Appl
	6	269.8	98.8	1440	13	US-10-138-888-12	Sequence 12, Appl
	7	263	96.3	10825	13	US-10-138-888-79	GENERAL INFORMA
	8	261.4	95.8	5982	14	US-10-016-634A-25	Sequence 25, Appl
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	10	261.4	95.8	10825	13	US-10-138-888-3	GENERAL INFORMA
	11	261.4	95.8	12146	13	US-09-981-606-27	Sequence 27, Appl
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c	13	261.4	95.8	237326	15	US-10-301-844-2	Sequence 2, Appli
	14	259.8	95.2	10825	13	US-10-138-888-5	GENERAL INFORMA
	15	259.8	95.2	10825	13	US-10-138-888-7	GENERAL INFORMA
	16	259	94.9	596	12	US-10-158-057-105	Sequence 105, App
	17	98.4	36.0	100	13	US-10-272-665-110	Sequence 110, App
	18	98.4	36.0	100	13	US-10-273-321-110	Sequence 110, App
	19	98.4	36.0	100	13	US-10-272-756-110	Sequence 110, App
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	29	55.8	20.4	652	14	US-10-027-632-130688	Sequence 130688,
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	32	53.2	19.5	2053	13	US-09-814-353-20518	Sequence 20518, A
	33	51	18.7	51	10	US-09-901-956-7	Sequence 7, Appli
	34	48.2	17.7	430	13	US-10-263-828-21	Sequence 21, Appl
	35	45.8	16.8	1590	12	US-10-388-934-812	Sequence 812, App
	36	45.4	16.6	47	13	US-10-220-507-19	Sequence 19, Appl
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	45	41.8	15.3	4969	12	US-10-388-934-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-10-138-888-77
; Sequence 77, Application US/10138888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912

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;           FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Brian M. Poissant
;           REGISTRATION NUMBER: 28,462
;           REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 790-9090
;           TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 77:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1440 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;           NAME/KEY:  CDS
;           LOCATION:  222..1268
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;           LOCATION:  replace(414, "t")
;           OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;           (HH)"
;           /label= 24d7
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  Query Match             100.0%;  Score 273;  DB 13;  Length 1440;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-86;
  Matches  273;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        408 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 2
US-10-138-888-9
; Sequence 9, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Pennie & Edmonds LLP
;           STREET: 1155 Avenue of the Americas
;           CITY: New York
;           STATE: New York
;           COUNTRY: USA
;           ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/138,888
;           FILING DATE: 02-May-2002
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/834,497
;           FILING DATE: 04-APR-1997
;           APPLICATION NUMBER: US 08/652,265
;           FILING DATE: 23-MAY-1996
;           APPLICATION NUMBER: US 08/632,673
;           FILING DATE: 16-APR-1996
;           APPLICATION NUMBER: US 08/630,912
;           FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Brian M. Poissant
;           REGISTRATION NUMBER: 28,462
;           REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 790-9090
;           TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1440 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;           NAME/KEY:  CDS
;           LOCATION:  222..1268
;       FEATURE:
;           NAME/KEY:  allele
;           LOCATION:  replace(408, "c")
;           OTHER INFORMATION:  /phenotype= "normal or wild-type
;           (unaffected)"
;           /label= 24d2
;       FEATURE:
;           NAME/KEY:  allele
;           LOCATION:  replace(414, "a")
;           OTHER INFORMATION:  /phenotype= "normal or wild-type
;           (unaffected)"
;           /label= 24d7
;       FEATURE:
;           NAME/KEY:  allele
;           LOCATION:  replace(1066, "g")
;           OTHER INFORMATION:  /phenotype= "normal or wild-type
;           (unaffected)"
;           /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-138-888-9

  Query Match             99.4%;  Score 271.4;  DB 13;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 6.9e-86;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 3
US-10-138-888-10
; Sequence 10, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;    INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1440 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  222..1268
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(1066, "a")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d1
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-138-888-10

  Query Match           99.4%;  Score 271.4;  DB 13;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 6.9e-86;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 4
US-09-981-606-1
; Sequence 1, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg et al.
;  TITLE OF INVENTION: Mutations associated with iron disorders
;  FILE REFERENCE: 24065-004CON
;  CURRENT APPLICATION NUMBER: US/09/981,606
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2506
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-981-606-1

  Query Match           99.4%;  Score 271.4;  DB 13;  Length 2506;
  Best Local Similarity   99.6%;  Pred. No. 8.7e-86;
  Matches  272;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 126

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 186

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 246

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 306

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        307 TGGACTATTATGGAAAATCACAACCACAGCAAG 339


RESULT 5
US-10-138-888-11
; Sequence 11, Application US/10138888
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; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1440 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  222..1268
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(408, "g")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d2
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-138-888-11

  Query Match             98.8%;  Score 269.8;  DB 13;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.5e-85;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
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Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              ||||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 6
US-10-138-888-12
; Sequence 12, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1440 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  222..1268
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(408, "g")
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;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d2
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(1066, "a")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d1
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-138-888-12

  Query Match             98.8%;  Score 269.8;  DB 13;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.5e-85;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347

Qy         61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407

Qy        121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467

Qy        181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527

Qy        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||||||||||
Db        528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560


RESULT 7
US-10-138-888-79
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;             OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;             (HH) protein containing the 24d7 mutation"
;             /note= "Hereditary Hemochromatosis
;             (HH)gene 24d7 allele"
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  140..7319
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  5507..6023
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(3878, "t")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d7
;        SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-138-888-79

  Query Match             96.3%;  Score 263;  DB 13;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-82;
  Matches  263;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 3881

Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        251 TGGAAAATCACAACCACAGCAAG 273
              |||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAG 4024


RESULT 8
US-10-016-634A-25
; Sequence 25, Application US/10016634A
; Publication No. US20020192666A1
; GENERAL INFORMATION:
;  APPLICANT: Sun, Yongming
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Ghosh, Malavika
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Prc
;  FILE REFERENCE: DEX-0255
;  CURRENT APPLICATION NUMBER: US/10/016,634A
;  CURRENT FILING DATE:  2001-10-31
;  PRIOR APPLICATION NUMBER: US 60/244,258
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 176
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
;    LENGTH: 5982
;    TYPE: DNA
;    ORGANISM: Homo sapiens
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5780)..(5780)
;   OTHER INFORMATION: n=a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5885)..(5885)
;   OTHER INFORMATION: n=a, c, g or t
US-10-016-634A-25

  Query Match             95.8%;  Score 261.4;  DB 14;  Length 5982;
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  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
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Db        3402 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3461

Qy          71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        3462 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3521

Qy         131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Db        3522 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3581

Qy         191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3582 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 3641

Qy         251 TGGAAAATCACAACCACAGCAAG 273
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Db        3642 TGGAAAATCACAACCACAGCAAG 3664


RESULT 9
US-10-138-888-1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;            OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;            (HH) protein"
;            /note= "No. US20030148972A1mal or wild-type (unaffected)
;            Hereditary Hemochromatosis (HH) gene
;            allele"
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  140..7319
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  5507..6023
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(3878, "a")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d7
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(5834, "g")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-138-888-1

  Query Match             95.8%;  Score 261.4;  DB 13;  Length 10825;
  Best Local Similarity   99.6%;  Pred. No. 6.1e-82;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy          71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy         131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy         191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy         251 TGGAAAATCACAACCACAGCAAG 273
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Db        4002 TGGAAAATCACAACCACAGCAAG 4024


RESULT 10
US-10-138-888-3
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
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;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;            OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;            (HH) protein containing the 24d1
;            mutation"
;            /note= "Hereditary Hemochromatosis (HH)
;            gene 24d1 allele"
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  140..7319
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  5507..6023
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-138-888-3

  Query Match             95.8%;  Score 261.4;  DB 13;  Length 10825;
  Best Local Similarity   99.6%;  Pred. No. 6.1e-82;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy          71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy         131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Db        3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy         191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy         251 TGGAAAATCACAACCACAGCAAG 273
               |||||||||||||||||||||||
Db        4002 TGGAAAATCACAACCACAGCAAG 4024


RESULT 11
US-09-981-606-27
; Sequence 27, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg et al.
;  TITLE OF INVENTION: Mutations associated with iron disorders
;  FILE REFERENCE: 24065-004CON
;  CURRENT APPLICATION NUMBER: US/09/981,606
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 12146
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-981-606-27

  Query Match             95.8%;  Score 261.4;  DB 13;  Length 12146;
  Best Local Similarity   99.6%;  Pred. No. 6.4e-82;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
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Db        4652 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 4711

Qy          71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        4712 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 4771

Qy         131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Db        4772 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 4831

Qy         191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Db        4832 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4891

Qy         251 TGGAAAATCACAACCACAGCAAG 273
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Db        4892 TGGAAAATCACAACCACAGCAAG 4914


RESULT 12
US-10-301-844-1/c
; Sequence 1, Application US/10301844
; Publication No. US20030100747A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruddy, David A.
;                   Wolff, Roger K.
;        TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
;                            HEMOCHROMATOSIS GENE
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds, LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/301,844
;             FILING DATE: 20-No. US20030100747A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/852,495C
;             FILING DATE: 07-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-0057-999
;        TELECOMMUNICATION INFORMATION:
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```
;               TELEPHONE: 650-493-4935
;               TELEFAX: 650-493-5556
;               TELEX: 66141 PENNIE
;     INFORMATION FOR SEQ ID NO: 1:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 235033 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-301-844-1

  Query Match             95.8%;  Score 261.4;  DB 15;  Length 235033;
  Best Local Similarity   99.6%;  Pred. No. 2.4e-81;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db      43388 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 43329

Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
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Db      43328 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 43269

Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Db      43268 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 43209

Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Db      43208 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43149

Qy        251 TGGAAAATCACAACCACAGCAAG 273
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Db      43148 TGGAAAATCACAACCACAGCAAG 43126


RESULT 13
US-10-301-844-2/c
; Sequence 2, Application US/10301844
; Publication No. US20030100747A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruddy, David A.
;                   Wolff, Roger K.
;        TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
;                            HEMOCHROMATOSIS GENE
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds, LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/301,844
;             FILING DATE: 20-No. US20030100747A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/852,495C
;             FILING DATE: 07-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-0057-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;     INFORMATION FOR SEQ ID NO: 2:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 237326 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-301-844-2

  Query Match             95.8%;  Score 261.4;  DB 15;  Length 237326;
  Best Local Similarity   99.6%;  Pred. No. 2.4e-81;
  Matches  262;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db      43338 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 43279

Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
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Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Db      43218 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 43159

Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Db      43158 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43099

Qy        251 TGGAAAATCACAACCACAGCAAG 273
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Db      43098 TGGAAAATCACAACCACAGCAAG 43076


RESULT 14
US-10-138-888-5
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
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```
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;             OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;             (HH) protein containing the 24d2
;             mutation"
;             /note= "Hereditary Hemochromatosis (HH)
;             gene 24d2 allele"
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  140..7319
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  5507..6023
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-138-888-5

  Query Match             95.2%;  Score 259.8;  DB 13;  Length 10825;
  Best Local Similarity   99.2%;  Pred. No. 2.3e-81;
  Matches  261;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
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Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGATGAGAGTC 3881

Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        251 TGGAAAATCACAACCACAGCAAG 273
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Db       4002 TGGAAAATCACAACCACAGCAAG 4024


RESULT 15
US-10-138-888-7
;  GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;            OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;            (HH) protein containing both the 24d1
;            and 24d2 mutations"
;            /note= "Hereditary Hemochromatosis (HH)
;            gene containing a combination of both
;            24d1 and 24d2 alleles"
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;            NAME/KEY:  -
;            LOCATION:  140..7319
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  5507..6023
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(5834, "a")
;            OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;            (HH)"
;            /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-138-888-7

  Query Match             95.2%;  Score 259.8;  DB 13;  Length 10825;
  Best Local Similarity   99.2%;  Pred. No. 2.3e-81;
  Matches  261;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
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Qy        131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250
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Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        251 TGGAAAATCACAACCACAGCAAG 273
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Db       4002 TGGAAAATCACAACCACAGCAAG 4024


Search completed: February 11, 2004, 22:07:07
Job time : 236.656 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 15:39:51 ; Search time 904.219 Seconds
(without alignments)
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Perfect score: 151
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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35: em_htg_rod:*
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37: em_htg_vrt:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	150	99.3	360	6	AR097991	AR097991 Sequence
2	150	99.3	479	9	AF525359	AF525359 Homo sapi
3	150	99.3	517	6	AR117804	AR117804 Sequence
4	150	99.3	517	6	AR117805	AR117805 Sequence
5	150	99.3	517	6	AR149474	AR149474 Sequence
6	150	99.3	517	6	AR149475	AR149475 Sequence
7	150	99.3	517	6	I82157	I82157 Sequence 3
8	150	99.3	517	6	I82158	I82158 Sequence 4
9	150	99.3	517	6	I82167	I82167 Sequence 13
10	150	99.3	551	9	AF331065	AF331065 Homo sapi
11	150	99.3	653	9	HSHLAH4	Y09803 H.sapiens H
12	150	99.3	733	9	AF525499	AF525499 Homo sapi
13	150	99.3	772	9	AF184234	AF184234 Homo sapi
14	150	99.3	781	9	AF079409	AF079409 Homo sapi
15	150	99.3	809	9	HSA250635	AJ250635 Homo sapi
16	150	99.3	823	9	AF079408	AF079408 Homo sapi
17	150	99.3	860	9	AY205604	AY205604 Homo sapi
18	150	99.3	1045	9	AF079407	AF079407 Homo sapi
19	150	99.3	1073	9	HSA249337	AJ249337 Homo sapi
20	150	99.3	1085	9	HSA249336	AJ249336 Homo sapi
21	150	99.3	1200	9	AF115265	AF115265 Homo sapi
22	150	99.3	1280	9	HSA249335	AJ249335 Homo sapi
23	150	99.3	1317	6	AX407339	AX407339 Sequence
24	150	99.3	1440	6	AR117793	AR117793 Sequence
25	150	99.3	1440	6	AR117794	AR117794 Sequence
26	150	99.3	1440	6	AR117795	AR117795 Sequence
27	150	99.3	1440	6	AR117796	AR117796 Sequence
28	150	99.3	1440	6	AR149463	AR149463 Sequence
29	150	99.3	1440	6	AR149464	AR149464 Sequence
30	150	99.3	1440	6	AR149465	AR149465 Sequence
31	150	99.3	1440	6	AR149466	AR149466 Sequence
32	150	99.3	2506	6	AR199238	AR199238 Sequence
33	150	99.3	2506	6	AR275757	AR275757 Sequence
34	150	99.3	2727	9	HSU60319	U60319 Homo sapien
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36	150	99.3	10825	6	AR117790	AR117790 Sequence
37	150	99.3	10825	6	AR117791	AR117791 Sequence
38	150	99.3	10825	6	AR117792	AR117792 Sequence
39	150	99.3	10825	6	AR149459	AR149459 Sequence
40	150	99.3	10825	6	AR149460	AR149460 Sequence
41	150	99.3	10825	6	AR149461	AR149461 Sequence
42	150	99.3	10825	6	AR149462	AR149462 Sequence
c 43	150	99.3	11214	9	AF447807	AF447807 Pan trogl
44	150	99.3	12146	6	AR199263	AR199263 Sequence
45	150	99.3	12146	6	AR275782	AR275782 Sequence

ALIGNMENTS

RESULT 1
AR097991
LOCUS AR097991 360 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6074825.
ACCESSION AR097991
VERSION AR097991.1 GI:12807248
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 360)
AUTHORS Rundell,C.A. and Vary,C.P.H.
TITLE Stable encapsulated reference nucleic acid and method of making
JOURNAL Patent: US 6074825-A 5 13-JUN-2000;
FEATURES Location/Qualifiers

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     source          1. .360
                     /organism="unknown"
BASE COUNT       87 a     91 c    101 g     81 t
ORIGIN

  Query Match             99.3%;  Score 150;  DB 6;  Length 360;
  Best Local Similarity   99.3%;  Pred. No. 2e-36;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        114 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 173

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 233

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        234 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 264


RESULT 2
AF525359
LOCUS       AF525359                479 bp    DNA     linear   PRI 24-JUL-2002
DEFINITION  Homo sapiens hereditary hemochromatosis protein HLA-H precursor
            (HFE) gene, exon 4 and partial cds.
ACCESSION   AF525359
VERSION     AF525359.1  GI:21952517
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 479)
  AUTHORS   Kutlar,F., Glendenning,M. and Kutlar,A.
  TITLE     Heterozygote C-->G mutation in intron 3 of human hemachromatosis
            gene detected on a caucasian individual with beta-thalassemia trait
            due to codon 39 C-->T mutation of beta globin gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 479)
  AUTHORS   Kutlar,F., Glendenning,M. and Kutlar,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2002) Medicine/Hematology-Oncology/Hemoglobin DNA
            Laboratory, Medical College of Georgia, 15th Street, AC-1000,
            Augusta, GA 30912, USA
FEATURES             Location/Qualifiers
     source          1. .479
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p21.3"
                     /sex="male"
                     /cell_type="white blood cell"
     gene            <1. .>479
                     /gene="HFE"
     variation       50
                     /gene="HFE"
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     mRNA            <98. .>373
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ORIGIN

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  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 240

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 300

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        301 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 331


RESULT 3
AR117804
LOCUS       AR117804                517 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 20 from patent US 6140305.
ACCESSION   AR117804
VERSION     AR117804.1  GI:14098710
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 20 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="unknown"
BASE COUNT      126 a    120 c    147 g    124 t
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  Query Match             99.3%;  Score 150;  DB 6;  Length 517;
  Best Local Similarity   99.3%;  Pred. No. 2e-36;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db        303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333


RESULT 4
AR117805
LOCUS       AR117805                517 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 21 from patent US 6140305.
ACCESSION   AR117805
VERSION     AR117805.1  GI:14098711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 517)
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  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 21 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="unknown"
BASE COUNT      127 a    120 c    146 g    124 t
ORIGIN

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  Best Local Similarity   99.3%;  Pred. No. 2e-36;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||||| |||||
Db        303 CCTGGGGAAGAGCAGAGATATACGTACCAGG 333


RESULT 5
AR149474
LOCUS       AR149474                 517 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 20 from patent US 6228594.
ACCESSION   AR149474
VERSION     AR149474.1  GI:15114065
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 20 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="unknown"
BASE COUNT      126 a    120 c    147 g    124 t
ORIGIN

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  Best Local Similarity   99.3%;  Pred. No. 2e-36;
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Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333


RESULT 6
AR149475
LOCUS       AR149475                 517 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 21 from patent US 6228594.
ACCESSION   AR149475
VERSION     AR149475.1  GI:15114066
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 21 08-MAY-2001;
FEATURES             Location/Qualifiers
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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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RESULT 7
I82157
LOCUS       I82157                   517 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 3 from patent US 5712098.
ACCESSION   I82157
VERSION     I82157.1  GI:3210454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Tsuchihashi,Z., Gnirke,A., Thomas,W.J., Drayna,D.T., Ruddy,D.,
            Wolff,R.K. and Feder,J.N.
  TITLE     Hereditary hemochromatosis diagnostic markers and diagnostic
            methods
  JOURNAL   Patent: US 5712098-A 3 27-JAN-1998;
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ORIGIN

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333


RESULT 8
I82158
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LOCUS       I82158                  517 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 4 from patent US 5712098.
ACCESSION   I82158
VERSION     I82158.1  GI:3210455
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Tsuchihashi,Z., Gnirke,A., Thomas,W.J., Drayna,D.T., Ruddy,D.,
            Wolff,R.K. and Feder,J.N.
  TITLE     Hereditary hemochromatosis diagnostic markers and diagnostic
            methods
  JOURNAL   Patent: US 5712098-A 4 27-JAN-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      127 a    120 c    146 g    124 t
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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        303 CCTGGGGAAGAGCAGAGATATACGTACCAGG 333


RESULT 9
I82167
LOCUS       I82167                  517 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 13 from patent US 5712098.
ACCESSION   I82167
VERSION     I82167.1  GI:3210464
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Tsuchihashi,Z., Gnirke,A., Thomas,W.J., Drayna,D.T., Ruddy,D.,
            Wolff,R.K. and Feder,J.N.
  TITLE     Hereditary hemochromatosis diagnostic markers and diagnostic
            methods
  JOURNAL   Patent: US 5712098-A 13 27-JAN-1998;
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BASE COUNT      126 a    120 c    146 g    124 t      1 others
ORIGIN

  Query Match             99.3%;  Score 150;  DB 6;  Length 517;
  Best Local Similarity   100.0%;  Pred. No. 2e-36;
  Matches  151;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||||||||||
Db        303 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 333


RESULT 10
AF331065
LOCUS       AF331065                551 bp    DNA     linear   PRI 07-MAR-2001
DEFINITION  Homo sapiens hereditary hemochromatosis protein precursor (HFE)
            gene, exon 4 and partial cds.
ACCESSION   AF331065
VERSION     AF331065.1  GI:13241987
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   Kutlar,F., Holley,L., Glendenning,M. and Kutlar,A.
  TITLE     A new compound heterozygotes IVS4-48G/A/IVS4-115T/C polymorphism of
            HFE gene found in an Africa American individual with mild anemia
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 551)
  AUTHORS   Kutlar,F., Holley,L., Glendenning,M. and Kutlar,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-2000) Medicine/Hemoglobin DNA Laboratory; Sickle
            Cell Center, Medical College of Georgia, 15th street, AC-1000
            30912, USA
FEATURES             Location/Qualifiers
     source          1. .551
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p21.3"
                     /sex="male"
                     /cell_type="WBC"
                     /tissue_type="whole blood"
     gene            <1. .>551
                     /gene="HFE"
     intron          <1. .116
                     /gene="HFE"
                     /number=3
     mRNA            <117. .>392
                     /gene="HFE"
     CDS             <117. .>392
                     /gene="HFE"
                     /note="HLA-H precursor; putative iron-binding ligand
                     receptor"
                     /codon_start=3
                     /product="hereditary hemochromatosis protein precursor"
                     /protein_id="AAK16502.1"
                     /db_xref="GI:13241988"
                     /translation="PPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKE
                     FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIW"
     exon            117. .392
                     /gene="HFE"
                     /number=4
     intron          393. .551
                     /gene="HFE"
                     /number=4
     variation       440
                     /gene="HFE"
                     /note="heterozygous polymorphism"
                     /replace="g"
     variation       501
                     /gene="HFE"
                     /note="homozygous"
                     /replace="a"
     variation       507
                     /gene="HFE"
                     /note="heterozygous polymorphism"
                     /replace="t"
BASE COUNT      133 a    124 c    153 g    141 t
ORIGIN

Db        303 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 333
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  Query Match             99.3%;  Score 150;  DB 9;  Length 551;
  Best Local Similarity   99.3%;  Pred. No. 2e-36;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 259

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 319

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db        320 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 350


RESULT 11
HSHLAH4
LOCUS       HSHLAH4                   653 bp    DNA     linear   PRI 23-JUL-1999
DEFINITION  H.sapiens HFE gene, exon 4 & 5.
ACCESSION   Y09803
VERSION     Y09803.1  GI:2370113
KEYWORDS    HFE gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Carella and Gasparini,P.
  TITLE     Hereditary hemochromatosis genomic structure and organization of
            HLA-H gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 653)
  AUTHORS   Gasparini,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-DEC-1996) P. Gasparini, Servizio de Genetica Medica -
            IRCCS, 'Ospedale CSS', Via Cappuccini, 71013 S Giovanni, Rotondo
            (FG), ITALY
COMMENT     Related sequence: U60319.
FEATURES             Location/Qualifiers
     source          1. .653
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="6p22"
                     /clone_lib="31H6"
     gene            51. .598
                     /gene="HFE"
     exon            51. .326
                     /gene="HFE"
                     /usedin=Y09801:hfe_cds
                     /usedin=Y09801:hfe_mrna
                     /label=ex4
     exon            485. .598
                     /gene="HFE"
                     /usedin=Y09801:hfe_cds
                     /usedin=Y09801:hfe_mrna
                     /label=ex5
BASE COUNT      154 a    140 c    190 g    168 t      1 others
ORIGIN

  Query Match             99.3%;  Score 150;  DB 9;  Length 653;
  Best Local Similarity   99.3%;  Pred. No. 2e-36;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 193

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        194 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 253

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db        254 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 284


RESULT 12
AF525499
LOCUS       AF525499                  733 bp    DNA     linear   PRI 04-AUG-2002
DEFINITION  Homo sapiens hereditary hemochromatosis protein precursor (HFE)
            gene, partial cds.
ACCESSION   AF525499
VERSION     AF525499.1  GI:22094648
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 733)
  AUTHORS   Kutlar,F., Glendenning,M. and Kutlar,A.
  TITLE     Heterozygote T->C mutation was detected at the intron 4 of the
            human hemachromatosis gene in an Africa American individual
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 733)
  AUTHORS   Kutlar,F., Glendenning,M. and Kutlar,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2002) Medicine/Hematology-Oncology/Hemoglobin DNA
            Laboratory, Medical College of Georgia, 15th street, AC-1000,
            Augusta, GA 30912, USA
FEATURES             Location/Qualifiers
     source          1. .733
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /isolation_source="African-American individual"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p21.3"
                     /sex="female"
                     /cell_type="WBC"
     gene            <1. .>733
                     /gene="HFE"
                     /note="synonym: HLA-H"
     mRNA            join(<114. .389,548. .>661)
                     /gene="HFE"
     CDS             join(<114. .389,548. .>661)
                     /gene="HFE"
                     /note="HLA-H protein precursor"
                     /codon_start=3
                     /product="hereditary hemochromatosis protein precursor"
                     /protein_id="AAM91950.1"
                     /db_xref="GI:22094649"
                     /translation="PPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKE
                     FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIG
                     VISGIAVFVVILFIGILFIILRKRQGS"
     exon            114. .389
                     /gene="HFE"
                     /number=4
     variation       498
                     /gene="HFE"
                     /note="homozygote"
                     /replace="a"
     variation       504
                     /gene="HFE"
                     /note="heterozygote"
                     /replace="t"
     exon            548. .661
                     /gene="HFE"
                     /number=5
BASE COUNT      176 a    159 c    211 g    187 t
ORIGIN

  Query Match             99.3%;  Score 150;  DB 9;  Length 733;
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  Best Local Similarity   99.3%;  Pred. No. 2e-36;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 256

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 316

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db        317 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 347


RESULT 13
AF184234
LOCUS       AF184234                772 bp    DNA     linear   PRI 05-OCT-1999
DEFINITION  Homo sapiens hereditary haemochromatosis protein precursor (HFE)
            gene, partial cds.
ACCESSION   AF184234
VERSION     AF184234.1  GI:6010710
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   Kutlar,F., Sromek,E., Holley,L., Leithner,C., Nechtman,J. and
            Kutlar,A.
  TITLE     Two different mutations found in intron 4 of the human
            hemochromatosis gene, in a Turkish family
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 772)
  AUTHORS   Kutlar,F., Sromek,E., Holley,L., Leithner,C., Nechtman,J. and
            Kutlar,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-1999) Medicine/Hematology/Oncology/Sickle Cell
            Center, Medical College of Georgia, 15 th St., AC-1000, Augusta, GA
            30912, USA
FEATURES             Location/Qualifiers
     source          1. .772
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p21.3"
                     /cell_type="white blood cell"
     gene            <1. .>772
                     /gene="HFE"
     mRNA            join(<130. .405,564. .>677)
                     /gene="HFE"
                     /product="hereditary haemochromatosis protein precursor"
     CDS             join(<130. .405,564. .>677)
                     /gene="HFE"
                     /note="type I membrane protein; HLA-H"
                     /codon_start=3
                     /product="hereditary haemochromatosis protein precursor"
                     /protein_id="AAF01222.1"
                     /db_xref="GI:6010711"
                     /translation="PPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKE
                     FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIG
                     VISGIAVFVVILFIGILFIILRKRQGS"
     exon            130. .405
                     /gene="HFE"
                     /number=4
     variation       453
                     /gene="HFE"
                     /note="heterzygous"
                     /replace="g"
     variation       514
                     /gene="HFE"
                     /note="homozygous"
                     /replace="a"
     exon            564. .677
                     /gene="HFE"
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BASE COUNT      183 a    167 c    219 g    203 t
ORIGIN

  Query Match           99.3%;  Score 150;  DB 9;  Length 772;
  Best Local Similarity   99.3%;  Pred. No. 2e-36;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 272

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 332

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db        333 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 363


RESULT 14
AF079409
LOCUS       AF079409                781 bp    mRNA    linear   PRI 18-MAR-1999
DEFINITION  Homo sapiens Hemochromatosis splice variant delE2(14E4) (HFE) mRNA,
            complete cds.
ACCESSION   AF079409
VERSION     AF079409.1  GI:3695110
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   Rhodes,D.A. and Trowsdale,J.
  TITLE     Alternate splice variants of the hemochromatosis gene Hfe
  JOURNAL   Immunogenetics 49 (4), 357-359 (1999)
  MEDLINE   99180629
   PUBMED   10079302
REFERENCE   2  (bases 1 to 781)
  AUTHORS   Rhodes,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-1998) Immunology, University of Cambridge, Tennis
            Court Road, Cambridge CB2 1QP, UK
FEATURES             Location/Qualifiers
     source          1. .781
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p22.1"
     gene            1. .781
                     /gene="HFE"
     CDS             37. .777
                     /gene="HFE"
                     /codon_start=1
                     /product="hemochromatosis splice variant delE214E4"
                     /protein_id="AAC62648.1"
                     /db_xref="GI:3695111"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLQSHTLQVILGCEMQEDNST
                     EGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQ
                     LQQLLELGRGVLDQQVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG
                     TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIGVISGIAVFVVIL
                     FIGILFIILRKRQGSRGAMGHYVLAERE"
BASE COUNT      185 a    197 c    244 g    155 t
ORIGIN

  Query Match           99.3%;  Score 150;  DB 9;  Length 781;
  Best Local Similarity   99.3%;  Pred. No. 2e-36;
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Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 489

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 549

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||||| |||||
Db        550 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 580


RESULT 15
HSA250635
LOCUS       HSA250635               809 bp    mRNA    linear   PRI 03-NOV-2001
DEFINITION  Homo sapiens mRNA for Hemochromatosis protein (HFE gene), DELEX2+3
            splice form.
ACCESSION   AJ250635
VERSION     AJ250635.1  GI:16751450
KEYWORDS    alternative splicing; hemochromatosis protein; HFE gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sanchez,M. and Oliva,R.
  TITLE     Identification of different alternative splicing forms of the HFE
            gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 809)
  AUTHORS   Oliva,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-1999) Oliva R., Human Genome Research Group,
            Faculty of Medicine and Clinic Hospital, Casanova 143, 08036, SPAIN
FEATURES             Location/Qualifiers
     source          1. .809
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
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                     /cell_line="HepG2"
     gene            1. .809
                     /gene="HFE"
     CDS             161. .667
                     /gene="HFE"
                     /note="alternative splicing, exons 2 and 3 are not
                     present"
                     /codon_start=1
                     /evidence=experimental
                     /product="Hemochromatosis protein"
                     /protein_id="CAC80805.1"
                     /db_xref="GI:16751451"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLLPPLVKVTHHVTSSVTTLR
                     CRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTC
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                     HYVLAERE"
BASE COUNT      192 a    202 c    225 g    190 t
ORIGIN

  Query Match             99.3%;  Score 150;  DB 9;  Length 809;
  Best Local Similarity   99.3%;  Pred. No. 2e-36;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 379

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        380 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 439

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||||| |||||
Db        440 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 470


Search completed: February 11, 2004, 19:15:41
Job time : 905.219 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 15:39:52 ; Search time 861.127 Seconds
(without alignments)
4261.827 Million cell updates/sec

Title: 09981606-1B_COPY_700_850
Perfect score: 151
Sequence: 1 aacatcaccatgaagtggct.....gcagagatatacgtnccagg 151

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	150	99.3	668	12	BM723847	BM723847 UI-E-EO1-
c	3	150	99.3	729	14	CB529554	CB529554 UI-H-FT2-
	4	126	83.4	819	10	BG747345	BG747345 602704818
c	5	84.4	55.9	444	28	AZ025590	AZ025590 RPCI-23-3
	6	84.4	55.9	1719	11	AK088986	AK088986 Mus muscu
	7	84.4	55.9	1723	11	AK009581	AK009581 Mus muscu
	8	73.6	48.7	831	12	BI452668	BI452668 603169877
c	9	70.8	46.9	536	28	AZ074871	AZ074871 RPCI-23-4
c	10	65.6	43.4	481	28	AZ025784	AZ025784 RPCI-23-3
c	11	52.2	34.6	473	12	BM781326	BM781326 MLN1_7_F0
	12	50.8	33.6	2338	11	AK030695	AK030695 Mus muscu
	13	50.8	33.6	2490	11	AK029010	AK029010 Mus muscu
	14	49.8	33.0	752	29	AB005947	AB005947 Mouse gen
	15	48.4	32.1	710	14	CB466784	CB466784 732494 MA
	16	48.2	31.9	550	10	BF118828	BF118828 601755052
	17	48.2	31.9	952	13	BQ889432	BQ889432 AGENCOURT
	18	48	31.8	529	14	CB221873	CB221873 1IL21A5 B
c	19	48	31.8	553	10	BF828080	BF828080 MR1-HN007
	20	48	31.8	557	14	CB222669	CB222669 1IL30E11
	21	47.8	31.7	490	10	BE487497	BE487497 176270 BA
c	22	47.4	31.4	1142	13	BX437832	BX437832 BX437832
	23	47	31.1	341	10	BG694169	BG694169 345218 BA
	24	46.6	30.9	491	12	BI042832	BI042832 RC5-OT009
	25	46.6	30.9	495	9	AA475498	AA475498 vh15f05.r
c	26	46.6	30.9	676	14	CB530229	CB530229 737006 MA
	27	46.6	30.9	727	14	CB593814	CB593814 AGENCOURT
	28	46.6	30.9	916	12	BI660863	BI660863 603303915
	29	46.6	30.9	937	12	BI559071	BI559071 603241545
	30	46.6	30.9	978	12	BI854358	BI854358 603381312
	31	46.4	30.7	218	10	BF741057	BF741057 QV1-HB003
	32	46.4	30.7	230	10	BF171757	BF171757 PCL3324 M
	33	46.4	30.7	372	12	BM430293	BM430293 1Duo32E10
	34	46.4	30.7	405	10	BG690430	BG690430 338970 BA
	35	46.4	30.7	411	10	BE487675	BE487675 176738 BA
	36	46.4	30.7	431	14	CB222620	CB222620 1IL29H11
	37	46.4	30.7	445	12	BM430459	BM430459 1Duo34F2.
	38	46.4	30.7	453	10	BE480812	BE480812 166048 BA
	39	46.4	30.7	457	14	CB465504	CB465504 727553 MA
	40	46.4	30.7	458	10	BE479563	BE479563 164308 BA
	41	46.4	30.7	459	9	AW652180	AW652180 100012 MA
	42	46.4	30.7	460	10	BE478603	BE478603 162929 BA
	43	46.4	30.7	461	12	BM433103	BM433103 1A22E12 B
	44	46.4	30.7	488	10	BE845698	BE845698 232986 BA
	45	46.4	30.7	490	10	BE478472	BE478472 162741 BA

ALIGNMENTS

RESULT 1
BE272926
LOCUS BE272926 570 bp mRNA linear EST 13-JUL-2000
DEFINITION 601171213F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3544803 5', mRNA sequence.
ACCESSION BE272926
VERSION BE272926.1 GI:9147279
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 570)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM240 row: j column: 04
High quality sequence stop: 566.
FEATURES Location/Qualifiers

```
     source          1. .570
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3544803"
                     /tissue_type="renal cell adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_14"
                     /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      140 a    148 c    175 g    107 t
ORIGIN

  Query Match             99.3%;  Score 150;  DB 10;  Length 570;
  Best Local Similarity   99.3%;  Pred. No. 5.8e-33;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 469

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 529

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db        530 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 560


RESULT 2
BM723847
LOCUS       BM723847                668 bp    mRNA    linear   EST 01-MAR-2002
DEFINITION  UI-E-EO1-aix-h-17-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone
            UI-E-EO1-aix-h-17-0-UI 5', mRNA sequence.
ACCESSION   BM723847
VERSION     BM723847.1  GI:19045178
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 668)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .668
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EO1-aix-h-17-0-UI"
                     /tissue_type="fetal eye"
                     /dev_stage="fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-EO1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EO1 is a normalized cDNA library containing the
                     following tissue(s): fetal eye. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CGCGTATACC. This library was created for the program, Gene
                     Discovery in the Visual System, supported by National Eye
                     Institute (NEI)."
BASE COUNT      164 a    166 c    167 g    171 t
ORIGIN

  Query Match             99.3%;  Score 150;  DB 12;  Length 668;
  Best Local Similarity   99.3%;  Pred. No. 6.2e-33;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 93

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 153

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db        154 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 184


RESULT 3
CB529554/c
LOCUS       CB529554                729 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  UI-H-FT2-bjh-m-12-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjh-m-12-0-UI 3', mRNA sequence.
ACCESSION   CB529554
VERSION     CB529554.1  GI:29390357
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 729)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
```

```
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjh-m-12-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     subtracted according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. The tissue was provided by Dr.
                     Gary W. Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT2
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      151 a    211 c    165 g    202 t
ORIGIN

  Query Match             99.3%;  Score 150;  DB 14;  Length 729;
  Best Local Similarity   99.3%;  Pred. No. 6.4e-33;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 428

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 368

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db        367 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 337


RESULT 4
BG747345
LOCUS       BG747345                 819 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602704818F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857941 5',
            mRNA sequence.
ACCESSION   BG747345
VERSION     BG747345.1  GI:14057998
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1711  row: d  column: 06
            High quality sequence stop: 792.
FEATURES             Location/Qualifiers
     source          1. .819
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4857941"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_15"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT      202 a    201 c    235 g    181 t
ORIGIN

  Query Match             83.4%;  Score 126;  DB 10;  Length 819;
  Best Local Similarity   98.0%;  Pred. No. 5.7e-26;
  Matches  148;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        537 AACATCACCATGAAGTGGCTGAAGGATAAGCAG-CAATGGATGCCAAGGAGTTCGAACCT 595

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        596 AAAGACGTATTGCCCAATGGGGATGGGACCTACCA-GGCTGGATAACCTTGGCTGTACCC 654

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db        655 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 685


RESULT 5
AZ025590/c
LOCUS       AZ025590                 444 bp    DNA     linear   GSS 25-FEB-2000
DEFINITION  RPCI-23-316A10.TV RPCI-23 Mus musculus genomic clone RPCI-23-316A10
            , genomic survey sequence.
ACCESSION   AZ025590
VERSION     AZ025590.1  GI:7100974
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 444)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 316  row: A  column: 10
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .444
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-316A10"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
```

EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "

BASE COUNT 110 a 126 c 110 g 97 t 1 others
ORIGIN

Query Match 55.9%; Score 84.4; DB 28; Length 444;
Best Local Similarity 72.2%; Pred. No. 4.6e-14;
Matches 109; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

```
Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||  ||||  ||||  |||||||  ||  ||  |||  ||||||||||  ||   ||  |  ||
Db        241 AACATCACTATGAGGTGGTTGAAGGACAACCAACCACTGGATGCCAAAGATGTCAACCCC 182

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                |  | ||   | ||  ||  |||||||  ||||||  ||  ||||||  ||||   ||||  ||   ||
Db        181 GAGAAGGTGCTACCTAACGGGGATGAGACCTATCAAGGCTGGCTAACAATGGCCGTGGCC 122

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||  |||   ||  |  ||  |  ||  |
Db        121 CCTGGGGACGAGACAAGGTTCACCTGTCAAG 91
```

RESULT 6
AK088986
LOCUS AK088986 1719 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430034J19 product:hemochromatosis, full insert sequence.
ACCESSION AK088986
VERSION AK088986.1 GI:26354115
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1719)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES Location/Qualifiers
source 1. .1719
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/strain="NOD"
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/db_xref="taxon:10090"
/clone="E430034J19"
/cell_type="thymic cells"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="2 days neonate"
CDS 97. .1173
/note="unnamed protein product; hemochromatosis (MGD|MGI:109191)
putative"
/codon_start=1

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                     VDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWRYGYDGQDHLEFC
                     PKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLELGRGVLGQQVP
                     TLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVLPNGDETYQ
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ORIGIN

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  Best Local Similarity   72.2%;  Pred. No. 7.8e-14;
  Matches  109;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              |||||||| |||| |||| ||||||| || || ||| |||||||||| ||  || | ||
Db        829 AACATCACTATGAGGTGGTTGAAGGACAACCAACCACTGGATGCCAAAGATGTCAACCCC 888

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
               |  | ||  |||| || || |||| |||||| || |||||| | || |||||  ||   ||
Db        889 GAGAAGGTGCTGCCTAACGGAGATGAGACCTATCAAGGCTGGCTGACGTTGGCAGTGGCC 948

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||  |||   ||  |  ||  |  || |
Db        949 CCTGGGGACGAGACAAGGTTCACCTGTCAAG 979


RESULT 7
AK009581
LOCUS       AK009581               1723 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
            library, clone:2310032M04 product:hemochromatosis, full insert
            sequence.
ACCESSION   AK009581
VERSION     AK009581.1  GI:12844462
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1723)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
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                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
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                     /note="unnamed protein product; hemochromatosis
                     (MGD|MGI:109191)
                     putative"
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                     CPKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLELGRGVLGQQV
                     PTLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVLPNGDETY
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ORIGIN

  Query Match             55.9%;  Score 84.4;  DB 11;  Length 1723;
  Best Local Similarity   72.2%;  Pred. No. 7.8e-14;
  Matches  109;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db        834 AACATCACTATGAGGTGGTTGAAGGACAACCAACCACTGGATGCCAAAGATGTCAACCCC 893

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                | | ||  | || || ||||||| |||||| || |||||| | || ||||| ||  ||
Db        894 GAGAAGGTGCTACCTAACGGGGATGAGACCTATCAAGGCTGGCTGACATTGGCCGTGGCC 953

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||| |||   || |  || |  || |
Db        954 CCTGGGGACGAGACAAGGTTCACCTGTCAAG 984


RESULT 8
BI452668
LOCUS       BI452668                 831 bp    mRNA    linear   EST 21-AUG-2001
DEFINITION  603169877F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5249395 5',
            mRNA sequence.
ACCESSION   BI452668
VERSION     BI452668.1  GI:15243324
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 831)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11629  row: j  column: 20
            High quality sequence stop: 818.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5249395"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="7 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam5"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH"
BASE COUNT      207 a    220 c    189 g    215 t
ORIGIN

  Query Match             48.7%;  Score 73.6;  DB 12;  Length 831;
  Best Local Similarity   70.8%;  Pred. No. 7.7e-11;
  Matches   97;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

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Db          2 GTGGTTGAAGGACAACCAACCACTGGATGCCAAAGATGTCAACCCCGAGAAGGTGCTACC 61

Qy         75 CAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCA 134
                || ||||||| |||||| || |||||| | || ||||| ||  |||||||||| |||
Db         62 TAACGGGGATGAGACCTATCAAGGCTGGCTGACATTGGCCGTGGCCCCTGGGGACGAGAC 121

Qy        135 GAGATATACGTNCCAGG 151
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Db        122 AAGGTTCACCTGTCAAG 138


RESULT 9
AZ074871/c
LOCUS       AZ074871                 536 bp    DNA     linear   GSS 31-MAR-2000
DEFINITION  RPCI-23-408J22.TJ RPCI-23 Mus musculus genomic clone RPCI-23-408J22
            , genomic survey sequence.
ACCESSION   AZ074871
VERSION     AZ074871.1  GI:7367768
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 536)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished
COMMENT     Other_GSSs: RPCI-23-408J22.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 408  row: J  column: 22
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="RPCI-23-408J22"
/sex="Female"
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/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
BASE COUNT 148 a 149 c 124 g 114 t 1 others
ORIGIN

Query Match 46.9%; Score 70.8; DB 28; Length 536;
Best Local Similarity 70.9%; Pred. No. 4.2e-10;
Matches 107; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

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Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db        258 AACATCACTATGAGGTGGTTGAAGGACAACCAACCACTGGATGCCAAAGATGTCAACCCC 199

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
               |  | ||  | || || ||||||| |||||| || ||||||||  | ||  | ||  ||
Db        198 GAGAAGGTGCTACCTAACGGGGATGAGACCTATCAAGGCTGGAT-GCATTAACCGTGGCC 140

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||| |||   || |  || |  || |
Db        139 CCTGGGGACGAGACAAGGTTCACCTGTCAAG 109
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RESULT 10
AZ025784/c
LOCUS AZ025784 481 bp DNA linear GSS 25-FEB-2000
DEFINITION RPCI-23-316C10.TV RPCI-23 Mus musculus genomic clone RPCI-23-316C10 , genomic survey sequence.
ACCESSION AZ025784
VERSION AZ025784.1 GI:7101168
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 481)
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished
COMMENT Other_GSSs: RPCI-23-316C10.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 316 row: C column: 10
Seq primer: T7
Class: BAC ends.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-316C10"
/sex="Female"
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/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
BASE COUNT 126 a 135 c 112 g 108 t
ORIGIN

Query Match 43.4%; Score 65.6; DB 28; Length 481;
Best Local Similarity 68.9%; Pred. No. 1.3e-08;
Matches 104; Conservative 0; Mismatches 45; Indels 2; Gaps 1;

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Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db        257 AACATCACTATGAGGTGGTTGAAGGACAACCAACCACTGGATGCCAAAGATGTCAACCCC 198

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
               |  | ||  | || || ||||||| |||||| || ||||||| |||     |   ||  ||
Db        197 GAGAAGGTGCTACCTAACGGGAATGAGACCTATCAAGGCTGGCTAA--AAGAAAGTGGCC 140

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||| |||   || |  || |  || |
Db        139 CCTGGGGACGAGACAAGGTTCACCTGTCAAG 109
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RESULT 11
BM781326/c
LOCUS BM781326 473 bp mRNA linear EST 05-MAR-2002
DEFINITION MLN1_7_F05.g1_A005 Mesenteric lymph node (MLN1) Equus caballus cDNA , mRNA sequence.
ACCESSION BM781326
VERSION BM781326.1 GI:19129558
KEYWORDS EST.
SOURCE Equus caballus (horse)
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 473)
AUTHORS Watson,J.L., Vandenplas,M., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Moore,J. and Pratt,L.H.
TITLE An EST database from equine (Equus caballus) mesenteric lymph nodes
JOURNAL Unpublished
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. The cDNAs were cloned non-directionally such that the primer used for sequencing has no bearing on whether it is a 3' or 5' sequence.
Seq primer: T7
High quality sequence start: 2
High quality sequence stop: 473
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .473
/organism="Equus caballus"
/mol_type="mRNA"
/db_xref="taxon:9796"
/clone_lib="Mesenteric lymph node (MLN1)"
/note="Organ: Mesenteric lymph node; Vector: pBluescript SK(-) from Lambda ZapII; Site_1: EcoRI; Site_2: EcoRI; The

library was made from poly-A RNA in the cloning vector lambda ZAPII. Clones to be sequenced were prepared by mass excision."
BASE COUNT 103 a 147 c 132 g 91 t
ORIGIN

Query Match 34.6%; Score 52.2; DB 12; Length 473;
Best Local Similarity 59.6%; Pred. No. 9.4e-05;
Matches 87; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

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Qy          6 CACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGA 65
              |||  |||  |||||   ||||  | |||| ||| |         || |  ||||  |
Db        361 CACTCTGACCTGGCTTCTGGATGGGGAGCCCATGCACCAGGGCACCTTTGGGCCTAGGGC 302

Qy         66 CGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGG 125
              | |  |||||| |||||| |||||||||||  |||| |  ||        |  ||||  |
Db        301 CATCCTGCCCAGTGGGGACGGGACCTACCAGACCTGGGTGGCCACTCGGATCTCCCCCAG 242

Qy        126 GGAAGAGCAGAGATATACGTNCCAGG 151
                || |||||||  |   | | ||| |
Db        241 AGAGGAGCAGAATTTCGCCTCCCATG 216
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RESULT 12
AK030695
LOCUS AK030695 2338 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 10 days neonate head cDNA, RIKEN full-length enriched library, clone:5530400I18 product:hypothetical Major histocompatibility complex protein, Class I containing protein, full insert sequence.
ACCESSION AK030695
VERSION AK030695.1 GI:26326680
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2338)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES Location/Qualifiers
source 1. .2338
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:5530400I18"
/db_xref="taxon:10090"
/clone="5530400I18"
/tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 days neonate"
CDS 188. .1375
/note="unnamed protein product; hypothetical Major histocompatibility complex protein, Class I containing protein (InterPro|IPR001039, evidence: InterPro) putative"
/codon_start=1
/protein_id="BAC27084.1"
/db_xref="GI:26326681"
/translation="MLLSRNLRALAAIHLWIVYLLLEDLLGTCAEGDNQRLVASAPYQ
DIEITLEKPRVQALAEPHTLRYDLMALSLEVPGLPQFLTLRYFDDEPFLPYKKNSSIT
DSQEPRIKDHLRAETWGRETDDLQEEEEQLKGMLAEITAQNGQNTDLHILQATFGCEL
QRNGSTRGFWKLGYDGQNFLTFDQKTLTWTVDGPSTQKNKTLWKTRAPRADLVKAFLD

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                     DICPAQLQRYLASLRNGLLNTGFPKVIVTFRNYPVGRITLTCRAFRLYTRVATLTWLQ
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                     PVYGARREQPPTSGVGSRVGKSLWSAMTTALVVISWTLSQKLMGPLLWFCSGGFCSFL
                     QCW"
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                     /note="putative"
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BASE COUNT      686 a    541 c    534 g    577 t
ORIGIN

  Query Match             33.6%;  Score 50.8;  DB 11;  Length 2338;
  Best Local Similarity   62.7%;  Pred. No. 0.00044;
  Matches   79;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          6 CACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGA 65
              |||| |||  |||||  || |||   ||||| |  |    ||    || | | || ||
Db        997 CACCCTGACCTGGCTTCAGTATAGAAAGCCAGTACAGCAGAAAACCTTTGGATCTGAAAC 1056

Qy         66 CGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGG 125
                |  |||||| ||||||||| |||||||||| |||| |  || |    || |  |||||
Db       1057 TATCCTGCCCAGTGGGGATGGCACCTACCAGGCCTGGGTGTCCATTCGGGTTCTTCCTGG 1116

Qy         126 GGAAGA 131
                | ||
Db       1117 ACAGGA 1122


RESULT 13
AK029010
LOCUS       AK029010               2490 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
            library, clone:4732481C10 product:hypothetical Major
            histocompatibility complex protein, Class I containing protein,
            full insert sequence.
ACCESSION   AK029010
VERSION     AK029010.1  GI:26324971
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2490)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
     source          1. .2490
                     /organism="Mus musculus"
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                     /strain="C57BL/6J"
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                     /db_xref="taxon:10090"
                     /clone="4732481C10"
                     /tissue_type="skin"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="10 days neonate"
     CDS             265. .1452
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                     /note="putative"
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ORIGIN

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  Best Local Similarity  62.7%;  Pred. No. 0.00045;
  Matches   79;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          6 CACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGA 65
              |||| |||  |||||  || |||   ||||| |  |    ||    || | | || ||
Db       1074 CACCCTGACCTGGCTTCAGTATAGAAAGCCAGTACAGCAGAAAACCTTTGGATCTGAAAC 1133

Qy         66 CGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGG 125
                |  |||||| ||||||||| |||||||||| |||| |  || |    || |  |||||
Db       1134 TATCCTGCCCAGTGGGGATGGCACCTACCAGGCCTGGGTGTCCATTCGGGTTCTTCCTGG 1193

Qy        126 GGAAGA 131
                | ||
Db       1194 ACAGGA 1199


RESULT 14
AB005947
LOCUS       AB005947                752 bp    DNA     linear   GSS 04-AUG-1997
DEFINITION  Mouse genomic DNA, chromosome 17, clone cosmid 12.1, genomic survey
            sequence.
ACCESSION   AB005947
VERSION     AB005947.1  GI:2309033
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Yoshino,M., Jones,E. and Fischer Lindahl,K.
  TITLE     BAC clones from the H2-T region of the 129 mouse, Tlaf
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 752)
  AUTHORS   Yoshino,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUL-1997) Masayasu Yoshino, U.T. Southwestern Medical
            Center, HHMI; 5323 Harry Hines Blvd, Dallas, TX 75235-9050, USA
            (E-mail:YOSHINO@UTSW.SWMED.EDU, Tel:214-648-5047, Fax:214-648-5453)
FEATURES             Location/Qualifiers
     source          1. .752
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:10090"
                     /chromosome="17"
                     /clone="cosmid 12.1"
                     /haplotype="H2d"
                     /note="primer pTL5'(5'-cgcttccatcagcgtttatag)"
BASE COUNT      161 a    196 c    198 g    192 t      5 others
ORIGIN

  Query Match            33.0%;  Score 49.8;  DB 29;  Length 752;
  Best Local Similarity  62.7%;  Pred. No. 0.00055;
  Matches   94;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy          2 ACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTA 61
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Db        224 ACCTCACCCTGACCTGGCAGAAGGATGGGGAGGAGCTG---ACCCAGGACATGGAGTTTG 280

Qy         62 AAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCC 121
               |||       |||     |||||||| |||| ||||    |||  | |  |||  || || |
Db        281 TAGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTC 340

Qy        122 CTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                |||| |||||||||| || || | ||| |
Db        341 TTGGGAAAGAGCAGAGTTACACATGCCATG 370


RESULT 15
CB466784
LOCUS       CB466784                710 bp    mRNA    linear   EST 26-MAR-2003
DEFINITION  732494 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB466784
VERSION     CB466784.1  GI:29273169
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: LAM8009  row: C  column: 12
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .710
                     /organism="Bos taurus"
                     /mol_type="mRNA"
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                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
BASE COUNT      154 a    205 c    249 g    102 t
ORIGIN

  Query Match            32.1%;  Score 48.4;  DB 14;  Length 710;
  Best Local Similarity  65.4%;  Pred. No. 0.0014;
  Matches   70;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy         44 CCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGA 103
               || ||||  | || | |   ||       |||    |||||||| |||| ||||   |||
Db        593 CCCAGGACATGGAGCTTGTGGAGACCAGGCCTTCAGGGGATGGAACCTTCCAGAAGTGGG 652

Qy        104 TAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTNCCAG 150
              | || |||| || ||  |||| || ||||||||||| |||| || |
Db        653 CAGCCCTGGCGGTGCCTTCTGGAGAGGAGCAGAGATACACGTGCCCG 699


Search completed: February 11, 2004, 19:57:36
Job time : 864.127 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 15:39:51 ; Search time 111.113 Seconds
(without alignments)
3668.467 Million cell updates/sec

Title: 09981606-1B_COPY_700_850
Perfect score: 151
Sequence: 1 aacatcaccatgaagtggct.....gcagagatatacgtnccagg 151

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*
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21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	150	99.3	359	20	AAX16055	Hereditary hemochr
	2	150	99.3	517	22	AAC68440	Human hereditary h
	3	150	99.3	517	22	AAC68441	Human hereditary h
	4	150	99.3	1317	24	ABK49917	DNA encoding beta
	5	150	99.3	1440	18	AAT96691	Hereditary haemoch
	6	150	99.3	1440	22	AAC68429	Human hereditary h
	7	150	99.3	1440	22	AAC68430	Human hereditary h
	8	150	99.3	1440	22	AAC68431	Human hereditary h
	9	150	99.3	1440	22	AAC68432	Human hereditary h
	10	150	99.3	2506	21	AAA96769	cDNA sequence enco
	11	150	99.3	2727	19	AAV23525	Haemochromatosis g
	12	150	99.3	5749	22	AAL36747	Human musculoskele
	13	150	99.3	5749	25	ABX59735	cDNA encoding nove
	14	150	99.3	10825	18	AAT96690	Hereditary haemoch
	15	150	99.3	10825	22	AAC68425	Human hereditary h
	16	150	99.3	10825	22	AAC68426	Human hereditary h
	17	150	99.3	10825	22	AAC68427	Human hereditary h
	18	150	99.3	10825	22	AAC68428	Human hereditary h
	19	150	99.3	12146	21	AAA96794	Genomic DNA of a h
c	20	150	99.3	235033	19	AAV57926	Hereditary haemoch
c	21	148.4	98.3	237326	19	AAV57903	Hereditary haemoch
c	22	51	33.8	76	22	AAF58226	Oligonucleotide D1
c	23	51	33.8	76	22	AAF58227	Oligonucleotide D1
	24	50.4	33.4	148834	24	ABK83570	Human cDNA differe
	25	50	33.1	100	22	AAH02415	Human HLA-H exon 4
	26	50	33.1	100	22	AAH02416	Human HLA-H exon 4
	27	45	29.8	300	24	ABQ78762	Differentially exp
	28	45	29.8	4756	22	AAI63974	Human polynucleoti
	29	45	29.8	4756	22	AAI63975	Human polynucleoti
	30	44.8	29.7	434	25	ABX39656	Bovine EST associa
	31	44.8	29.7	1101	12	AAQ12117	HLA-C exon Cb-2.
	32	44.8	29.7	1377	25	ABX63563	Human cDNA #563 di
	33	44.8	29.7	1554	22	AAI93004	Human polynucleoti
c	34	44.8	29.7	2225	24	ABZ11436	Human polynucleoti
	35	44.8	29.7	3372	22	AAI63979	Human polynucleoti
	36	44.8	29.7	3372	22	AAI64011	Human polynucleoti
c	37	44.6	29.5	305	22	ABA51289	Human breast cell
c	38	44.6	29.5	305	22	ABA69295	Human foetal liver
c	39	44.6	29.5	305	22	ABA36224	Probe #14690 for g
c	40	44.6	29.5	305	22	AAK17581	Human brain expres
c	41	44.6	29.5	305	22	AAK43395	Human bone marrow
c	42	44.6	29.5	305	22	AAI24176	Probe #14109 for g
c	43	44.6	29.5	305	22	AAI49463	Probe #18149 used
c	44	44.6	29.5	305	22	AAI09738	Probe #9729 used t
c	45	44.6	29.5	305	23	ABS43016	Human liver single

ALIGNMENTS

RESULT 1
AAX16055
ID AAX16055 standard; DNA; 359 BP.
XX
AC AAX16055;
XX
DT 19-MAY-1999 (first entry)
XX
DE Hereditary hemochromatosis gene target nucleic acid sequence.
XX
KW Hereditary hemochromatosis gene; encapsulate; lipoprotein outer membrane;
KW membrane stability; test cell; molecular diagnosis; genetic testing; ss.
XX
OS Unidentified.
XX
PN WO9906594-A1.
XX
PD 11-FEB-1999.
XX
PF 29-JUL-1998; 98WO-US15641.
XX
PR 23-DEC-1997; 97US-0997522.
PR 31-JUL-1997; 97US-0905124.
XX
PA (MAIN-) MAINE MEDICAL CENT.
XX
PI Rundell CA, Vary CPH;
XX
DR WPI; 1999-153816/13.
XX
PT Biological preparation of a stably encapsulated reference nucleic

PT acid - useful for molecular diagnostic and genetic testing
XX
PS Claim 5; Page 48; 51pp; English.
XX
CC The present sequence represents a nucleic acid sequence that is used as
CC a reference sequence to exemplify the method of the invention. The
CC specification describes a method for the biological preparation of a
CC stably encapsulated reference nucleic acid for molecular diagnostic and
CC genetic testing. The method comprises inserting a vector containing a
CC reference nucleic acid into a cell through its lipoprotein outer membrane
CC to encapsulate the nucleic acid, multiplying the cell to propagate the
CC nucleic acid, inducing cell death without affecting the nucleic acid,
CC and achieving a desired stability of the cell membrane for substantially
CC matching the nucleic acid with the membrane stability of test cells. The
CC reference nucleic acids are useful for molecular diagnosis and genetic
CC testing.
XX
SQ Sequence 359 BP; 86 A; 91 C; 101 G; 81 T; 0 other;

Query Match 99.3%; Score 150; DB 20; Length 359;
Best Local Similarity 99.3%; Pred. No. 1.1e-39;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 233

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db        234 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 264
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RESULT 2
AAC68440
ID AAC68440 standard; DNA; 517 BP.
XX
AC AAC68440;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis DNA used for mutation detection.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ss.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 6; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 517 BP; 126 A; 120 C; 147 G; 124 T; 0 other;

Query Match 99.3%; Score 150; DB 22; Length 517;
Best Local Similarity 99.3%; Pred. No. 1.2e-39;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333
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RESULT 3
AAC68441
ID AAC68441 standard; DNA; 517 BP.
XX
AC AAC68441;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis DNA used for mutation detection.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ss.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 6; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 517 BP; 127 A; 120 C; 146 G; 124 T; 0 other;

```
  Query Match           99.3%;  Score 150;  DB 22;  Length 517;
  Best Local Similarity  99.3%;  Pred. No. 1.2e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db        303 CCTGGGGAAGAGCAGAGATATACGTACCAGG 333


RESULT 4
ABK49917
ID   ABK49917 standard; cDNA; 1317 BP.
XX
AC   ABK49917;
XX
DT   15-JUL-2002  (first entry)
XX
DE   DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
XX
KW   Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
KW   iron absorption regulator; intracellular iron absorption; lung injury;
KW   haemochromatosis; transfusion; thalassaemia; haemolytic anaemia;
KW   chronic infection; transferrin receptor; TfR; brain tumour; cancer;
KW   oxidative stress disorder; tissue damage; vascular disease;
KW   inflammation; atherosclerosis; autoimmune disease;
KW   inflammatory condition; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1317
FT                   /*tag=  a
FT                   /product= "beta2M/HFE monochain"
XX
PN   WO200224929-A2.
XX
PD   28-MAR-2002.
XX
PF   24-SEP-2001; 2001WO-US29873.
XX
PR   22-SEP-2000; 2000US-234843P.
XX
PA   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA   (MCIN/) MCINNIS P.
XX
PI   Ehrlich R,  Rotem-Yehudar R,  Laham N;
XX
DR   WPI; 2002-383192/41.
DR   P-PSDB; AAU80035.
XX
PT   Soluble beta 2 microglobulin/HFE monochain useful for treating
PT   iron-overload conditions e.g. thalassemia and chronic infections,
PT   comprises human beta 2 microglobulin linked to alpha domains of HFE by
PT   a linker peptide  -
XX
PS   Example 2; Fig 2; 77pp; English.
XX
CC   The invention relates to a soluble polypeptide (I) of beta 2
CC   microglobulin (beta2m)/HFE monochain comprising human beta2m (or its
CC   analogue or active fragment), linked to alpha1-alpha3 domains of human
CC   HFE (a central regulator of iron absorption; undefined), or its analogue
CC   or active fragment, by a flexible linker peptide, or a functional
CC   derivative or salt of (I). (I) is useful for reducing intracellular iron
CC   absorption in patients having hereditary haemochromatosis, transfusions,
CC   thalassaemias, haemolytic anaemia or chronic infections, and for
CC   delivering a therapeutic to cells that over-express transferrin receptor
CC   (TfR) which are preferably lymphocytes or leukocytes, across the blood-
CC   brain barrier. (I) is further useful for treating brain tumour. (I)
CC   is also useful for treating oxidative stress disorders resulting in
CC   tissue damage e.g. vascular diseases, inflammation, atherosclerosis,
CC   lung injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful
CC   as a platform for drug delivery of therapeutic use for cancer,
CC   autoimmune diseases and inflammatory conditions. The monochain manifests
CC   specific characteristics advantageous for drug delivery systems. It is a
CC   soluble, stable and fully conformed protein. It binds specifically to
CC   transferrin receptor (TfR) and therefore targets cells that over-express
CC   this receptor. It is continuously internalised by the target cells, thus
CC   enabling efficient drug delivery. It dissociates from the receptor in the
CC   cells, minimising side effects. It negatively regulates iron absorption,
CC   reducing growth of undesired cells and preventing lymphocyte activation.
CC   It is not diluted in the blood as is transferrin. It should not induce an
CC   immune response since it is a self non-polymeric protein and delivery of
CC   drugs via monochain is expected to overcome drug-resistance since it is a
CC   natural TfR-binding protein. The present sequence represents the
CC   coding sequence of beta2m/HFE monochain.
XX
SQ   Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;

  Query Match           99.3%;  Score 150;  DB 24;  Length 1317;
  Best Local Similarity  99.3%;  Pred. No. 1.6e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1155

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db       1156 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1186


RESULT 5
AAT96691
ID   AAT96691 standard; cDNA; 1440 BP.
XX
AC   AAT96691;
XX
DT   14-APR-1998  (first entry)
XX
DE   Hereditary haemochromatosis gene cDNA clone.
XX
KW   Hereditary haemochromatosis; metal toxicity; diagnosis;
KW   gene therapy; prenatal screening; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             222.1268
FT                   /*tag=  a
FT   mutation        408
FT                   /*tag=  g
FT                   /note= "C to G substitution (24d2 mutation)
FT                          results in His to Asp substitution"
FT   variation       414
FT                   /*tag=  h
FT                   /note= "A to T substitution (24d7 variant)
FT                          results in Ser to Cys substitution"
FT   mutation        1066
FT                   /*tag=  i
FT                   /note= "G to A substitution (24d1 mutation
FT                          associated with HH), results in Cys to
FT                          Tyr substitution"
XX
```

```
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US06254.
XX
PR   23-MAY-1996;   96US-0652265.
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   P-PSDB; AAW36499.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis
PT   and treatment of hereditary haemochromatosis disease
XX
PS   Disclosure; Fig 4; 115pp; English.
XX
CC   This cDNA clone, designated cDNA24, is derived from human gene
CC   whose mutated form is associated with hereditary haemochromatosis
CC   (HH). It was obtained from a directionally cloned plasmid-based
CC   cDNA library following identification of the HH locus in the HLA
CC   region of chromosome 6. A single mutation (24d1) in the HH gene
CC   appears responsible for the majority of HH disease. This comprises
CC   a G to A substitution that is present in 86% of affected
CC   chromosomes and in 4% of unaffected chromosomes. It results in a
CC   Cys to Tyr substitution in the encoded protein (see AAW36499) at a
CC   critical disulphide bridge important for secondary structure. The
CC   following are claimed: a 10825 bp genomic DNA sequence (I) (see
CC   AAT96690), the 1437 bp cDNA sequence (Ia) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a
CC   peptide product chosen from the HH gene product, its variants
CC   (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC   residues of these; an antibody produced using the peptide; a method
CC   to determine the presence or absence of the common HH gene
CC   mutation; an animal model for the HH disease; metal chelation
CC   agents, T-cell differentiation factors and therapeutic agents for
CC   the mitigation of injury due to oxidative process in vivo or
CC   mitigation of iron overload; a method for screening potential
CC   therapeutic agents for activity in connection with HH disease; an
CC   antisense oligonucleotide directed against a transcriptional
CC   product of a nucleic acid sequence as above; and oligonucleotides
CC   or pairs of oligonucleotides covering a range of nucleotides from
CC   (I), (Ia) or their variants, useful for detecting a polymorphism in
CC   the HH gene. The invention also relates to methods for screening
CC   for HH homozygotes, to HH diagnosis, prenatal screening and
CC   diagnosis, and therapies of HH disease, including gene therapy,
CC   protein- and antibody-based therapeutics, and small molecule
CC   therapeutics.
XX
SQ   Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

  Query Match             99.3%;  Score 150;  DB 18;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071
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RESULT 6
AAC68429
ID   AAC68429 standard; DNA; 1440 BP.
XX
AC   AAC68429;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

  Query Match             99.3%;  Score 150;  DB 22;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071


RESULT 7
AAC68430
ID   AAC68430 standard; DNA; 1440 BP.
XX
AC   AAC68430;
XX
DT   21-FEB-2001  (first entry)
XX
```

```
DE   Human hereditary hemochromatosis 24d1 mutation cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;

  Query Match             99.3%;  Score 150;  DB 22;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTACCAGG 1071


RESULT 8
AAC68431
ID   AAC68431 standard; DNA; 1440 BP.
XX
AC   AAC68431;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d2 mutation cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 347 A; 354 C; 408 G; 331 T; 0 other;

  Query Match             99.3%;  Score 150;  DB 22;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071


RESULT 9
AAC68432
ID   AAC68432 standard; DNA; 1440 BP.
XX
AC   AAC68432;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d1/2 mutation cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
```

```
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 348 A; 354 C; 407 G; 331 T; 0 other;

  Query Match             99.3%;  Score 150;  DB 22;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTACCAGG 1071


RESULT 10
AAA96769
ID   AAA96769 standard; cDNA; 2506 BP.
XX
AC   AAA96769;
XX
DT   19-FEB-2001  (first entry)
XX
DE   cDNA sequence encoding a histocompatibility iron loading (HFE) protein.
XX
KW   Human; histocompatibility iron loading protein; HFE protein;
KW   major histocompatibility complex; non-classical class I gene;
KW   chromosome 6p; iron disorder; haemochromatosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1044
FT                   /*tag=  a
FT                   /product= "histocompatibility iron loading (HFE) protein"
FT   sig_peptide     1..66
FT                   /*tag=  b
FT   mutation        187
FT                   /*tag=  c
FT                   /note= "if this base is mutated to G, then the
FT                          protein contains the mutation H63D"
FT   mutation        193
FT                   /*tag=  d
FT                   /note= "if this base is mutated to T, then the
FT                          protein contains the mutation S65C"
FT   mutation        277
FT                   /*tag=  e
FT                   /note= "if this base is mutated to C, then the
FT                          protein contains the mutation G93R"
FT   mutation        314
FT                   /*tag=  f
FT                   /note= "if this base is mutated to C, then the
FT                          protein contains the mutation I105T, which
FT                          is associated with an iron overload disorder"
XX
PN   WO200058515-A1.
XX
PD   05-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US07982.
XX
PR   26-MAR-1999;   99US-0277457.
XX
PA   (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI   Rothenberg BE,  Sawada-Hirai R,  Barton JC;
XX
DR   WPI; 2000-647244/62.
DR   P-PSDB; AAB19149.
XX
PT   Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT   susceptibility to develop it, by determining the presence of a mutation
PT   in exon 2 or an intron of a histocompatibility iron loading nucleic
PT   acid -
XX
PS   Disclosure; Page 2-3; 55pp; English.
XX
CC   The present sequence encodes a human histocompatibility iron loading
CC   (HFE) protein. The HFE gene is a major histocompatibility (MHC)
CC   non-classical class I gene located on chromosome 6p. Mutations in the
CC   gene lead to iron disorders. The specification describes a method for
CC   diagnosing an iron disorder or a genetic susceptibility to develop the
CC   disorder in a mammal. The method comprises determining the presence of
CC   a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
CC   is not a C to G missense mutation at nucleotide 187 of the sequence
CC   given in A96769 (Genbank Accession number U60319). The presence of the
CC   mutation indicates the disorder or the genetic susceptibility to the
CC   disorder. The method is used to diagnose an iron disorder
CC   e.g. haemochromatosis, or a genetic susceptibility to develop it.
XX
SQ   Sequence 2506 BP; 648 A; 552 C; 596 G; 710 T; 0 other;

  Query Match             99.3%;  Score 150;  DB 21;  Length 2506;
  Best Local Similarity   99.3%;  Pred. No. 1.9e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 759

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 819

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db        820 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 850


RESULT 11
AAV23525
ID   AAV23525 standard; mRNA; 2727 BP.
XX
AC   AAV23525;
XX
DT   10-JUL-1998  (first entry)
XX
DE   Haemochromatosis gene.
XX
KW   Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
KW   autosomal recessive disorder; ss.
XX
OS   Homo sapiens.
```

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XX
PN   WO9807884-A1.
XX
PD   26-FEB-1998.
XX
PF   22-AUG-1997;   97WO-AU00539.
XX
PR   03-SEP-1996;   96AU-0002083.
PR   23-AUG-1996;   96AU-0001849.
XX
PA   (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI   Busfield F,  Cullen LM,  Jazwinska EC,  Powell LW;
XX
DR   WPI; 1998-179064/16.
XX
PT   Detection of autosomal recessive disorder - particularly hereditary
PT   haemochromatosis, by detecting a mutation in the HC gene
XX
PS   Disclosure; Page -; 32pp; English.
XX
CC   This sequence represents the haemochromatosis (HC) gene. Mutations in
CC   this sequence are detected using the method of the invention. The method
CC   is for identifying an individual with hereditary haemochromatosis (HH) or
CC   a predisposition to develop HH or to genetically pass on HH to an
CC   offspring, comprising isolating a biological sample and amplifying a
CC   region of genomic DNA in the biological sample encompassing all or part
CC   of the DNA between markers D6S265 and D6S276, and detecting at least one
CC   homozygous or heterozygous mutation in a nucleotide within the region.
CC   The method can also be used for identifying an individual with an
CC   autosomal recessive disorder (ARD) or predisposition to develop and/or
CC   genetically pass on an ARD to an offspring, comprises isolating a
CC   biological sample from the individual and screening genomic DNA in the
CC   sample for the presence of a homozygous or heterozygous mutation in a
CC   gene, the normal function of which, is required to prevent progression of
CC   the disorder. The method(s) can be used to identify individuals that are
CC   homozygous or heterozygous (carriers) for the mutation causing the ARD.
CC   Especially the method is used to diagnose HH or predisposition to HH by
CC   detecting a Cys282Tyr substitution. Individuals homozygous for this
CC   mutation have HH and heterozygotes are potential carriers of the
CC   disease.
XX
SQ   Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;

  Query Match             99.3%;  Score 150;  DB 19;  Length 2727;
  Best Local Similarity   99.3%;  Pred. No. 2e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071


RESULT 12
AAL36747
ID   AAL36747 standard; DNA; 5749 BP.
XX
AC   AAL36747;
XX
DT   08-JAN-2002  (first entry)
XX
DE   Human musculoskeletal system related polynucleotide SEQ ID NO 3112.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein;
KW   musculoskeletal system; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155367-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01338.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.
PR   07-JUL-2000; 2000US-0216880.
PR   11-JUL-2000; 2000US-0217487.
PR   11-JUL-2000; 2000US-0217496.
PR   14-JUL-2000; 2000US-0218290.
PR   26-JUL-2000; 2000US-0220963.
PR   26-JUL-2000; 2000US-0220964.
PR   14-AUG-2000; 2000US-0224518.
PR   14-AUG-2000; 2000US-0224519.
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PR   14-AUG-2000; 2000US-0225266.
PR   14-AUG-2000; 2000US-0225267.
PR   14-AUG-2000; 2000US-0225268.
PR   14-AUG-2000; 2000US-0225270.
PR   14-AUG-2000; 2000US-0225447.
PR   14-AUG-2000; 2000US-0225757.
PR   14-AUG-2000; 2000US-0225758.
PR   14-AUG-2000; 2000US-0225759.
PR   18-AUG-2000; 2000US-0226279.
PR   22-AUG-2000; 2000US-0226681.
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PR   30-AUG-2000; 2000US-0228924.
PR   01-SEP-2000; 2000US-0229287.
PR   01-SEP-2000; 2000US-0229343.
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PR   01-SEP-2000; 2000US-0229345.
PR   05-SEP-2000; 2000US-0229509.
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PR   06-SEP-2000; 2000US-0230437.
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PR   08-SEP-2000; 2000US-0231242.
PR   08-SEP-2000; 2000US-0231243.
PR   08-SEP-2000; 2000US-0231244.
PR   08-SEP-2000; 2000US-0231413.
PR   08-SEP-2000; 2000US-0231414.
PR   08-SEP-2000; 2000US-0232080.
PR   08-SEP-2000; 2000US-0232081.
PR   12-SEP-2000; 2000US-0231968.
PR   14-SEP-2000; 2000US-0232397.
PR   14-SEP-2000; 2000US-0232398.
PR   14-SEP-2000; 2000US-0232399.
PR   14-SEP-2000; 2000US-0232400.
PR   14-SEP-2000; 2000US-0232401.
PR   14-SEP-2000; 2000US-0233063.
PR   14-SEP-2000; 2000US-0233064.
PR   14-SEP-2000; 2000US-0233065.
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PR   21-SEP-2000; 2000US-0234223.
PR   21-SEP-2000; 2000US-0234274.
PR   25-SEP-2000; 2000US-0234997.
PR   25-SEP-2000; 2000US-0234998.
PR   26-SEP-2000; 2000US-0235484.
PR   27-SEP-2000; 2000US-0235834.
PR   27-SEP-2000; 2000US-0235836.
PR   29-SEP-2000; 2000US-0236327.
PR   29-SEP-2000; 2000US-0236367.
PR   29-SEP-2000; 2000US-0236368.
PR   29-SEP-2000; 2000US-0236369.
PR   29-SEP-2000; 2000US-0236370.
PR   02-OCT-2000; 2000US-0236802.
PR   02-OCT-2000; 2000US-0237037.
PR   02-OCT-2000; 2000US-0237038.
PR   02-OCT-2000; 2000US-0237039.
PR   02-OCT-2000; 2000US-0237040.
PR   13-OCT-2000; 2000US-0239935.
PR   13-OCT-2000; 2000US-0239937.
PR   20-OCT-2000; 2000US-0240960.
PR   20-OCT-2000; 2000US-0241221.
PR   20-OCT-2000; 2000US-0241785.
PR   20-OCT-2000; 2000US-0241786.
PR   20-OCT-2000; 2000US-0241787.
PR   20-OCT-2000; 2000US-0241808.
PR   20-OCT-2000; 2000US-0241809.
PR   20-OCT-2000; 2000US-0241826.
PR   01-NOV-2000; 2000US-0244617.
PR   08-NOV-2000; 2000US-0246474.
PR   08-NOV-2000; 2000US-0246475.
PR   08-NOV-2000; 2000US-0246476.
PR   08-NOV-2000; 2000US-0246477.
PR   08-NOV-2000; 2000US-0246478.
PR   08-NOV-2000; 2000US-0246523.
PR   08-NOV-2000; 2000US-0246524.
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PR   08-NOV-2000; 2000US-0246526.
PR   08-NOV-2000; 2000US-0246527.
PR   08-NOV-2000; 2000US-0246528.
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PR   17-NOV-2000; 2000US-0249209.
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PR   17-NOV-2000; 2000US-0249211.
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PR   17-NOV-2000; 2000US-0249244.
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PR   17-NOV-2000; 2000US-0249264.
PR   17-NOV-2000; 2000US-0249265.
PR   17-NOV-2000; 2000US-0249297.
PR   17-NOV-2000; 2000US-0249299.
PR   17-NOV-2000; 2000US-0249300.
PR   01-DEC-2000; 2000US-0250160.
PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
PR   05-DEC-2000; 2000US-0256719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
PR   08-DEC-2000; 2000US-0251868.
PR   08-DEC-2000; 2000US-0251869.
PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-451937/48.
XX
PT   Isolated polypeptide for treating, preventing and/ or prognosing
PT   disorders related to the musculoskeletal system including
PT   musculoskeletal cancers and also for testing and detection e.g.
PT   diagnosis -
XX
PS   Example 2; SEQ ID NO 3112; 781pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC   (ABB03087-ABB04109) associated with the musculoskeletal system useful
CC   for preventing, treating or ameliorating medical conditions e.g. by
CC   protein or gene therapy. The genes are isolated from a range of human
CC   tissues disclosed in the specification. The nucleic acids, proteins,
CC   antibodies and (ant)agonists are useful in the diagnosis, treatment
CC   and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC   other cancers of the adrenal gland, bone, bone marrow, breast,
CC   gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC   disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC   multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC   (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC   healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC   and (f) infectious diseases such as viral, bacterial, fungal and
CC   parasitic infections.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;

  Query Match             99.3%;  Score 150;  DB 22;  Length 5749;
  Best Local Similarity   99.3%;  Pred. No. 2.5e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db       1688 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 1747

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1748 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1807

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db       1808 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1838


RESULT 13
ABX59735
ID   ABX59735 standard; cDNA; 5749 BP.
XX
AC   ABX59735;
XX
DT   26-FEB-2003  (first entry)
XX
DE   cDNA encoding novel human musculoskeletal system antigen #2079.
XX
KW   Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW   re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KW   cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW   post-operative tissue repair; limb regeneration; neuronal growth;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   AIDS-related complex; chondrocyte growth; bone regeneration;
KW   periodontal regeneration; tissue transport; bone graft; skin aging;
```

KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW cell growth; organ transplant; cell differentiation; body height;
KW weight; hair colour; eye colour; skin; percentage of adipose tissue;
KW pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm;
KW depression; tendency for violence; pain; reproductive capability;
KW hormone level; endocrine level; appetite; libido; memory; stress;
KW storage capability; fat content; lipid content; protein content;
KW carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX
OS Homo sapiens.
XX
PN US2002147140-A1.
XX
PD 10-OCT-2002.
XX
PF 17-JAN-2001; 2001US-0764877.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226868P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234997P.
PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239935P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI; 2003-128199/12.
XX
PT Isolated nucleic acid molecules encoding musculoskeletal system
PT associated polypeptides, useful for detecting disorders, e.g. cancer -
XX
PS Disclosure; SEQ ID NO 3112; 321pp; English.
XX
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence encoding musculoskeletal system associated polypeptides useful
CC for detecting disorders, e.g., cancer or cancer metastases, in animals
CC or humans. The nucleic acid: stimulates re-vascularisation of ischaemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and
CC AIDS-related complex; stimulates chondrocyte growth, thus they can be
CC used to enhance bone and periodontal regeneration and aid in tissue
CC transports or bone grafts; prevents skin aging due to sunburn by
CC stimulating keratinocyte growth; prevents hair loss, since FGF family
CC members activate hair-forming cells and promotes melanocyte growth;
CC stimulates growth and differentiation of hematopoietic cells and bone
CC marrow cells when used in combination with other cytokines; maintains
CC organs before transplantation or for supporting cell culture of primary
CC tissues; induces tissue of mesodermal origin to differentiate in early
CC embryos; increases or decreases the differentiation or proliferation of
CC embryonic stem cells, besides, haematopoietic lineage; modulates
CC mammalian characteristics, such as, body height, weight, hair colour, eye
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes
CC mammal's metal state or physical state by influencing biorhythms,
CC caricadic rhythms, depression, tendency for violence, tolerance for pain,
CC reproductive capabilities, hormonal or endocrine levels, appetite,
CC libidc, memory, or stress; increases or decreases storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC or other nutritional components. This sequence encodes a novel human
CC musculoskeletal system antigen.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140.
XX
SQ Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;

Query Match 99.3%; Score 150; DB 25; Length 5749;
Best Local Similarity 99.3%; Pred. No. 2.5e-39;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
Db 1688 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 1747

Qy 61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
Db 1748 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1807

Qy 121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
Db 1808 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1838

RESULT 14
AAT96690
ID AAT96690 standard; DNA; 10825 BP.
XX
AC AAT96690;
XX
DT 14-APR-1998 (first entry)
XX
DE Hereditary haemochromatosis gene.

```
XX
KW   Hereditary haemochromatosis; metal toxicity; diagnosis;
KW   gene therapy; prenatal screening; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             361..7147
FT                   /*tag=  a
FT                   /note= "contains introns"
FT   intron          437..3761
FT                   /*tag=  b
FT                   /number= 1
FT   intron          4026..4234
FT                   /*tag=  c
FT                   /number= 2
FT   intron          4511..5605
FT                   /*tag=  d
FT                   /number= 3
FT   intron          5882..6039
FT                   /*tag=  e
FT                   /number= 4
FT   intron          6154..7106
FT                   /*tag=  f
FT                   /number= 5
FT   mutation        3872
FT                   /*tag=  g
FT                   /note= "C to G substitution (24d2 mutation)
FT                          results in His to Asp substitution"
FT   variation       3878
FT                   /*tag=  h
FT                   /note= "A to T substitution (24d7 variant)
FT                          results in Ser to Cys substitution"
FT   mutation        5834
FT                   /*tag=  i
FT                   /note= "G to A substitution (24d1 mutation
FT                          associated with HH), results in Cys to
FT                          Tyr substitution"
XX
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US06254.
XX
PR   23-MAY-1996;   96US-0652265.
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   P-PSDB; AAW36499.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis
PT   and treatment of hereditary haemochromatosis disease
XX
PS   Disclosure; Fig 3; 115pp; English.
XX
CC   This genomic DNA sequence corresponds to the human gene whose
CC   mutated form is associated with hereditary haemochromatosis (HH).
CC   To identify this novel gene, allelic association patterns were
CC   determined between known markers and the HH locus in the HLA region
CC   of chromosome 6.  A physical clone coverage was then generated
CC   extending from D6S265, which is a marker that is centromeric of
CC   HLA-A, in a telomeric direction through D6S276, a marker at which
CC   the allelic association was no longer observed.  A single mutation
CC   (24d1) in the HH gene appears responsible for the majority of HH
CC   disease.  This comprises a G to A substitution that is present in
CC   86% of affected chromosomes and in 4% of unaffected chromosomes.
CC   It results in a Cys to Tyr substitution in the encoded protein (see
CC   AAW36499) at a critical disulphide bridge important for secondary
CC   structure.  The following are claimed: the HH genomic DNA (I), a
CC   1437 bp cDNA sequence (Ia) (see AAT96691) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a
CC   peptide product chosen from the HH gene product, its variants
CC   (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC   residues of these; an antibody produced using the peptide; a method
CC   to determine the presence or absence of the common HH gene
CC   mutation; an animal model for the HH disease; metal chelation
CC   agents, T-cell differentiation factors and therapeutic agents for
CC   the mitigation of injury due to oxidative process in vivo or
CC   mitigation of iron overload; a method for screening potential
CC   therapeutic agents for activity in connection with HH disease; an
CC   antisense oligonucleotide directed against a transcriptional
CC   product of a nucleic acid sequence as above; and oligonucleotides
CC   or pairs of oligonucleotides covering a range of nucleotides from
CC   (I), (Ia) or their variants, useful for detecting a polymorphism in
CC   the HH gene.  The invention also relates to methods for screening
CC   for HH homozygotes, to HH diagnosis, prenatal screening and
CC   diagnosis, and therapies of HH disease, including gene therapy,
CC   protein- and antibody-based therapeutics, and small molecule
CC   therapeutics.
XX
SQ   Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;

  Query Match             99.3%;  Score 150;  DB 18;  Length 10825;
  Best Local Similarity   99.3%;  Pred. No. 2.9e-39;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5689 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 5748

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Db       5749 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 5808

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||||| |||||
Db       5809 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 5839


RESULT 15
AAC68425
ID   AAC68425 standard; DNA; 10825 BP.
XX
AC   AAC68425;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
```

DR WPI; 2001-006341/01.
DR P-PSDB; AAB36869.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;

Query Match 99.3%; Score 150; DB 22; Length 10825;
Best Local Similarity 99.3%; Pred. No. 2.9e-39;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5689 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 5748

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5749 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 5808

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db       5809 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 5839
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	150	99.3	1440	13	US-10-138-888-9	Sequence 9, Appli
4	150	99.3	1440	13	US-10-138-888-10	Sequence 10, Appl
5	150	99.3	1440	13	US-10-138-888-11	Sequence 11, Appl
6	150	99.3	1440	13	US-10-138-888-12	Sequence 12, Appl
7	150	99.3	1440	13	US-10-138-888-77	Sequence 77, Appl
8	150	99.3	2506	13	US-09-981-606-1	Sequence 1, Appli
9	150	99.3	5749	10	US-09-764-877-3112	Sequence 3112, Ap
10	150	99.3	5749	12	US-10-242-515-3112	Sequence 3112, Ap
11	150	99.3	10825	13	US-10-138-888-1	GENERAL INFORMA
12	150	99.3	10825	13	US-10-138-888-3	GENERAL INFORMA
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14	150	99.3	10825	13	US-10-138-888-7	GENERAL INFORMA
15	150	99.3	10825	13	US-10-138-888-79	GENERAL INFORMA
16	150	99.3	12146	13	US-09-981-606-27	Sequence 27, Appl
c 17	150	99.3	235033	15	US-10-301-844-1	Sequence 1, Appli
c 18	150	99.3	237326	15	US-10-301-844-2	Sequence 2, Appli
19	50	33.1	100	13	US-10-272-665-112	Sequence 112, App
20	50	33.1	100	13	US-10-272-665-113	Sequence 113, App
21	50	33.1	100	13	US-10-273-321-112	Sequence 112, App
22	50	33.1	100	13	US-10-273-321-113	Sequence 113, App
23	50	33.1	100	13	US-10-272-756-112	Sequence 112, App
24	50	33.1	100	13	US-10-272-756-113	Sequence 113, App
25	50	33.1	100	13	US-10-273-228-112	Sequence 112, App
26	50	33.1	100	13	US-10-273-228-113	Sequence 113, App
c 27	45	29.8	276	13	US-10-029-386-24031	Sequence 24031, A
28	45	29.8	300	9	US-09-854-124-17	Sequence 17, Appl
c 29	45	29.8	535	13	US-10-029-386-10322	Sequence 10322, A
30	45	29.8	535	13	US-10-029-386-11044	Sequence 11044, A
31	45	29.8	1139	13	US-09-971-429B-28	Sequence 28, Appl
32	45	29.8	4756	12	US-10-158-057-346	Sequence 346, App
33	45	29.8	4756	12	US-10-158-057-347	Sequence 347, App
34	44.8	29.7	276	13	US-10-029-386-18770	Sequence 18770, A
35	44.8	29.7	434	10	US-09-960-352-4821	Sequence 4821, Ap
36	44.8	29.7	484	11	US-09-918-995-32571	Sequence 32571, A
37	44.8	29.7	515	13	US-10-029-386-5014	Sequence 5014, Ap
c 38	44.8	29.7	554	13	US-10-029-386-2302	Sequence 2302, Ap
39	44.8	29.7	1377	14	US-10-044-090-563	Sequence 563, App
40	44.8	29.7	1533	13	US-09-971-429B-11	Sequence 11, Appl
41	44.8	29.7	3372	12	US-10-158-057-351	Sequence 351, App
42	44.8	29.7	3372	12	US-10-158-057-383	Sequence 383, App
c 43	44.6	29.5	301	13	US-10-029-386-19081	Sequence 19081, A
c 44	44.6	29.5	305	9	US-09-864-761-21544	Sequence 21544, A
45	44.6	29.5	321	9	US-09-962-436-311	Sequence 311, App

ALIGNMENTS

RESULT 1
US-10-138-888-20
; Sequence 20, Application US/10138888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912

```
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 20:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 517 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..517
;            OTHER INFORMATION:  /note= "normal or wild-type (unaffected)
;            genomic sequence surrounding variant for
;            24d1(G) allele corresponding to positions
;            5507-6023 of genomic sequence containing
;            the HH gene (SEQ ID NO:1)"
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(328, "g")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-138-888-20

  Query Match             99.3%;  Score 150;  DB 13;  Length 517;
  Best Local Similarity   99.3%;  Pred. No. 1.8e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||||| |||||
Db        303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333


RESULT 2
US-10-138-888-21
; Sequence 21, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 517 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..517
;            OTHER INFORMATION:  /note= "genomic sequence surrounding
;            variant for 24d1(A) allele corresponding
;            to positions 5507-6023 of genomic
;            sequence containing the HH gene
;            (SEQ ID NO:3)"
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(328, "a")
;            OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;            (HH)"
;            /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-138-888-21

  Query Match             99.3%;  Score 150;  DB 13;  Length 517;
  Best Local Similarity   99.3%;  Pred. No. 1.8e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        303 CCTGGGGAAGAGCAGAGATATACGTACCAGG 333


RESULT 3
US-10-138-888-9
; Sequence 9, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
```

```
;                 Tsuchihashi, Zenta
;                 Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1440 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  222..1268
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(408, "c")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d2
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(414, "a")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d7
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(1066, "g")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-138-888-9

  Query Match             99.3%;  Score 150;  DB 13;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||||| ||||

Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071


RESULT 4
US-10-138-888-10
; Sequence 10, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1440 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  222..1268
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(1066, "a")
;            OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;            (HH)"
;            /label= 24d1
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;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-138-888-10

  Query Match             99.3%;  Score 150;  DB 13;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTACCAGG 1071


RESULT 5
US-10-138-888-11
; Sequence 11, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1440 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  222..1268
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(408, "g")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d2
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-138-888-11

  Query Match             99.3%;  Score 150;  DB 13;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071


RESULT 6
US-10-138-888-12
; Sequence 12, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
```

```
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1440 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  222..1268
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(408, "g")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d2
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(1066, "a")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d1
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-138-888-12

  Query Match             99.3%;  Score 150;  DB 13;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db       1041 CCTGGGGAAGAGCAGAGATATACGTACCAGG 1071


RESULT 7
US-10-138-888-77
; Sequence 77, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 77:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1440 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  222..1268
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(414, "t")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d7
;        SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-138-888-77

  Query Match             99.3%;  Score 150;  DB 13;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071


RESULT 8
US-09-981-606-1
; Sequence 1, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg et al.
;  TITLE OF INVENTION: Mutations associated with iron disorders
;  FILE REFERENCE: 24065-004CON
;  CURRENT APPLICATION NUMBER: US/09/981,606
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2506
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-981-606-1
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  Best Local Similarity   99.3%;  Pred. No. 2.7e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db        700 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 759

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 819

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db        820 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 850


RESULT 9
US-09-764-877-3112
; Sequence 3112, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC005
;  CURRENT APPLICATION NUMBER: US/09/764,877
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 4031
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3112
;   LENGTH: 5749
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1222)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-764-877-3112

  Query Match             99.3%;  Score 150;  DB 10;  Length 5749;
  Best Local Similarity   99.3%;  Pred. No. 3.4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1688 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 1747

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1748 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1807

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db       1808 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1838


RESULT 10
US-10-242-515-3112
; Sequence 3112, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC005C1
;  CURRENT APPLICATION NUMBER: US/10/242,515
;  CURRENT FILING DATE:  2002-09-13
;  PRIOR APPLICATION NUMBER: 09/764,877
;  PRIOR FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: 60/179,065
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/180,628
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: 60/214,886
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/217,487
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,758
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/220,963
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/217,496
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,447
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/218,290
;  PRIOR FILING DATE: 2000-07-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4031
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3112
;   LENGTH: 5749
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1222)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-242-515-3112

  Query Match             99.3%;  Score 150;  DB 12;  Length 5749;
  Best Local Similarity   99.3%;  Pred. No. 3.4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db       1688 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 1747

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1748 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1807

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       1808 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1838


RESULT 11
US-10-138-888-1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;            OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;            (HH) protein"
;            /note= "No. US20030148972A1mal or wild-type (unaffected)
;            Hereditary Hemochromatosis (HH) gene
;            allele"
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  140..7319
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  5507..6023
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(3878, "a")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d7
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(5834, "g")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-138-888-1

  Query Match             99.3%;  Score 150;  DB 13;  Length 10825;
  Best Local Similarity   99.3%;  Pred. No. 4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db       5689 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 5748

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5749 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 5808

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       5809 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 5839


RESULT 12
US-10-138-888-3
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;            OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;            (HH) protein containing the 24d1
;            mutation"
;            /note= "Hereditary Hemochromatosis (HH)
;            gene 24d1 allele"
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  140..7319
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  5507..6023
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-138-888-3

  Query Match             99.3%;  Score 150;  DB 13;  Length 10825;
  Best Local Similarity   99.3%;  Pred. No. 4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5689 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 5748

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5749 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 5808

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       5809 CCTGGGGAAGAGCAGAGATATACGTACCAGG 5839


RESULT 13
US-10-138-888-5
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
```

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;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;         COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;         ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;         TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;             OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;             (HH) protein containing the 24d2
;             mutation"
;             /note= "Hereditary Hemochromatosis (HH)
;             gene 24d2 allele"
;         FEATURE:
;             NAME/KEY:  -
;             LOCATION:  140..7319
;         FEATURE:
;             NAME/KEY:  -
;             LOCATION:  5507..6023
;         SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-138-888-5

  Query Match             99.3%;  Score 150;  DB 13;  Length 10825;
  Best Local Similarity   99.3%;  Pred. No. 4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db       5689 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 5748

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5749 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 5808

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db       5809 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 5839


RESULT 14
US-10-138-888-7
;   GENERAL INFORMATION:
;         APPLICANT: Thomas, Winston J.
;                    Drayna, Dennis T.
;                    Feder, John N.
;                    Gnirke, Andreas
;                    Ruddy, David
;                    Tsuchihashi, Zenta
;                    Wolff, Roger K.
;         TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;         NUMBER OF SEQUENCES: 79
;         CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;         COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;         ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;         TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;             OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;             (HH) protein containing both the 24d1
;             and 24d2 mutations"
;             /note= "Hereditary Hemochromatosis (HH)
;             gene containing a combination of both
;             24d1 and 24d2 alleles"
;         FEATURE:
;             NAME/KEY:  -
;             LOCATION:  140..7319
;         FEATURE:
;             NAME/KEY:  -
;             LOCATION:  5507..6023
;         FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(5834, "a")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d1
;         SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-138-888-7

  Query Match             99.3%;  Score 150;  DB 13;  Length 10825;
  Best Local Similarity   99.3%;  Pred. No. 4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db       5689 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 5748

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Db       5749 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 5808

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db       5809 CCTGGGGAAGAGCAGAGATATACGTACCAGG 5839


RESULT 15
US-10-138-888-79
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;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;             OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;             (HH) protein containing the 24d7 mutation"
;             /note= "Hereditary Hemochromatosis
;             (HH)gene 24d7 allele"
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  140..7319
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  5507..6023
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(3878, "t")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d7
;        SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-138-888-79

  Query Match             99.3%;  Score 150;  DB 13;  Length 10825;
  Best Local Similarity   99.3%;  Pred. No. 4e-41;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db       5689 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 5748

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5749 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 5808

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||||| |||||
Db       5809 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 5839

Search completed: February 11, 2004, 22:07:08
Job time : 131.344 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: 09981606-1B_COPY_700_850
Perfect score: 151
Sequence: 1 aacatcaccatgaagtggct.....gcagagatatacgtnccagg 151

Scoring table: IDENTITY_NUC
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	150	99.3	360	3	US-08-905-124-5	Sequence 5, Appli
2	150	99.3	517	1	US-08-632-673B-3	Sequence 3, Appli
3	150	99.3	517	1	US-08-632-673B-4	Sequence 4, Appli
4	150	99.3	517	1	US-08-632-673B-13	Sequence 13, Appl
5	150	99.3	517	3	US-08-652-265-20	Sequence 20, Appl
6	150	99.3	517	3	US-08-652-265-21	Sequence 21, Appl
7	150	99.3	517	3	US-08-834-497A-20	Sequence 20, Appl
8	150	99.3	517	3	US-08-834-497A-21	Sequence 21, Appl
9	150	99.3	517	3	US-09-503-444A-20	Sequence 20, Appl
10	150	99.3	517	3	US-09-503-444A-21	Sequence 21, Appl
11	150	99.3	1440	3	US-08-652-265-9	Sequence 9, Appli
12	150	99.3	1440	3	US-08-652-265-10	Sequence 10, Appl
13	150	99.3	1440	3	US-08-652-265-11	Sequence 11, Appl
14	150	99.3	1440	3	US-08-652-265-12	Sequence 12, Appl
15	150	99.3	1440	3	US-08-834-497A-9	Sequence 9, Appli
16	150	99.3	1440	3	US-08-834-497A-10	Sequence 10, Appl
17	150	99.3	1440	3	US-08-834-497A-11	Sequence 11, Appl
18	150	99.3	1440	3	US-08-834-497A-12	Sequence 12, Appl
19	150	99.3	1440	3	US-09-503-444A-9	Sequence 9, Appli
20	150	99.3	1440	3	US-09-503-444A-10	Sequence 10, Appl
21	150	99.3	1440	3	US-09-503-444A-11	Sequence 11, Appl
22	150	99.3	1440	3	US-09-503-444A-12	Sequence 12, Appl
23	150	99.3	2506	4	US-09-277-457-1	Sequence 1, Appli
24	150	99.3	2506	4	US-09-679-729-1	Sequence 1, Appli
25	150	99.3	10825	3	US-08-652-265-1	Sequence 1, Appli
26	150	99.3	10825	3	US-08-652-265-3	Sequence 3, Appli
27	150	99.3	10825	3	US-08-652-265-5	Sequence 5, Appli
28	150	99.3	10825	3	US-08-652-265-7	Sequence 7, Appli
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32	150	99.3	10825	3	US-08-834-497A-7	Sequence 7, Appli
33	150	99.3	10825	3	US-09-503-444A-1	Sequence 1, Appli
34	150	99.3	10825	3	US-09-503-444A-3	Sequence 3, Appli
35	150	99.3	10825	3	US-09-503-444A-5	Sequence 5, Appli
36	150	99.3	10825	3	US-09-503-444A-7	Sequence 7, Appli
37	150	99.3	12146	4	US-09-277-457-27	Sequence 27, Appl
38	150	99.3	12146	4	US-09-679-729-27	Sequence 27, Appl
39	150	99.3	246240	2	US-08-724-394A-20	Sequence 20, Appl
40	150	99.3	246240	2	US-08-724-394A-21	Sequence 21, Appl
41	150	99.3	246240	2	US-08-724-394A-22	Sequence 22, Appl
42	45.2	29.9	1086	4	US-08-914-372C-1	Sequence 1, Appli
43	45.2	29.9	1086	4	US-08-914-372C-2	Sequence 2, Appli
44	45.2	29.9	1086	4	US-08-914-372C-3	Sequence 3, Appli
45	45.2	29.9	1086	4	US-08-914-372C-35	Sequence 35, Appl

ALIGNMENTS

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RESULT 1
US-08-905-124-5
; Sequence 5, Application US/08905124
; Patent No. 6074825
;  GENERAL INFORMATION:
;    APPLICANT:  Rundell, Clark A.
;    APPLICANT:  Vary, Calvin P.H.
;    TITLE OF INVENTION:  STABLE ENCAPSULTATED REFERENCE
;    TITLE OF INVENTION:  NUCLEIC ACID AND METHOD OF MAKING
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wood, Herron & Evans, L.L.P.
;      STREET:  2700 Carew Tower
;      CITY:  Cincinnati
;      STATE:  OH
;      COUNTRY:  USA
;      ZIP:  45202-2917
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows DEMONSTRATION Version 2.0D
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/905,124
;      FILING DATE:  31-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frei, Donald F
;      REGISTRATION NUMBER:  21,190
;      REFERENCE/DOCKET NUMBER:  CASI-02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  513-241-2324
;      TELEFAX:  513-421-7269
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  360 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;      CELL TYPE:  lymphocyte
US-08-905-124-5
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  Query Match             99.3%;  Score 150;  DB 3;  Length 360;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        114 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 173

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 233

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db        234 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 264


RESULT 2
US-08-632-673B-3
; Sequence 3, Application US/08632673B
; Patent No. 5712098
;  GENERAL INFORMATION:
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Wolff, Roger K.
;    APPLICANT:  Feder, John N.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS
;    TITLE OF INVENTION:  DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,673B
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  017957-000410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-632-673B-3

  Query Match             99.3%;  Score 150;  DB 1;  Length 517;
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Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||| |||||
Db        303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333


RESULT 3
US-08-632-673B-4
; Sequence 4, Application US/08632673B
; Patent No. 5712098
;  GENERAL INFORMATION:
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Wolff, Roger K.
;    APPLICANT:  Feder, John N.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS
;    TITLE OF INVENTION:  DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,673B
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  017957-000410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-632-673B-4

  Query Match             99.3%;  Score 150;  DB 1;  Length 517;
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  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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RESULT 4
US-08-632-673B-13
; Sequence 13, Application US/08632673B
; Patent No. 5712098
;  GENERAL INFORMATION:
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Wolff, Roger K.
;    APPLICANT:  Feder, John N.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS
;    TITLE OF INVENTION:  DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,673B
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  017957-000410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-632-673B-13

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  Best Local Similarity   100.0%;  Pred. No. 1.8e-43;
  Matches  151;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        303 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 333


RESULT 5
US-08-652-265-20
; Sequence 20, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..517
;      OTHER INFORMATION:  /note= "normal or wild-type (unaffected)
;      OTHER INFORMATION:  genomic sequence surrounding variant for
;      OTHER INFORMATION:  24d1(G) allele corresponding to positions
;      OTHER INFORMATION:  5507-6023 of genomic sequence containing
;      OTHER INFORMATION:  the HH gene (SEQ ID NO:1)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(328, "g")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-20

  Query Match             99.3%;  Score 150;  DB 3;  Length 517;
  Best Local Similarity   99.3%;  Pred. No. 1.8e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333
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RESULT 6
US-08-652-265-21
; Sequence 21, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..517
;      OTHER INFORMATION:  /note= "genomic sequence surrounding
;      OTHER INFORMATION:  variant for 24d1(A) allele corresponding
;      OTHER INFORMATION:  to positions 5507-6023 of genomic
;      OTHER INFORMATION:  sequence containing the HH gene
;      OTHER INFORMATION:  (SEQ ID NO:3)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(328, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-21

  Query Match             99.3%;  Score 150;  DB 3;  Length 517;
  Best Local Similarity   99.3%;  Pred. No. 1.8e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        303 CCTGGGGAAGAGCAGAGATATACGTACCAGG 333


RESULT 7
US-08-834-497A-20
; Sequence 20, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..517
;      OTHER INFORMATION:  /note= "normal or wild-type (unaffected)
;      OTHER INFORMATION:  genomic sequence surrounding variant for
;      OTHER INFORMATION:  24d1(G) allele corresponding to positions
;      OTHER INFORMATION:  5507-6023 of genomic sequence containing
;      OTHER INFORMATION:  the HH gene (SEQ ID NO:1)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(328, "g")
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;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-20

  Query Match             99.3%;  Score 150;  DB 3;  Length 517;
  Best Local Similarity   99.3%;  Pred. No. 1.8e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db        303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333


RESULT 8
US-08-834-497A-21
; Sequence 21, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..517
;      OTHER INFORMATION:  /note= "genomic sequence surrounding
;      OTHER INFORMATION:  variant for 24d1(A) allele corresponding
;      OTHER INFORMATION:  to positions 5507-6023 of genomic
;      OTHER INFORMATION:  sequence containing the HH gene
;      OTHER INFORMATION:  (SEQ ID NO:3)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(328, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-21

  Query Match             99.3%;  Score 150;  DB 3;  Length 517;
  Best Local Similarity   99.3%;  Pred. No. 1.8e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||| |||||
Db        303 CCTGGGGAAGAGCAGAGATATACGTACCAGG 333


RESULT 9
US-09-503-444A-20
; Sequence 20, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..517
;      OTHER INFORMATION:  /note= "normal or wild-type (unaffected)
;      OTHER INFORMATION:  genomic sequence surrounding variant for
;      OTHER INFORMATION:  24d1(G) allele corresponding to positions
;      OTHER INFORMATION:  5507-6023 of genomic sequence containing
;      OTHER INFORMATION:  the HH gene (SEQ ID NO:1)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(328, "g")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-09-503-444A-20

  Query Match             99.3%;  Score 150;  DB 3;  Length 517;
  Best Local Similarity   99.3%;  Pred. No. 1.8e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||||| |||||
Db        303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333


RESULT 10
US-09-503-444A-21
; Sequence 21, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..517
;      OTHER INFORMATION:  /note= "genomic sequence surrounding
;      OTHER INFORMATION:  variant for 24d1(A) allele corresponding
;      OTHER INFORMATION:  to positions 5507-6023 of genomic
;      OTHER INFORMATION:  sequence containing the HH gene
;      OTHER INFORMATION:  (SEQ ID NO:3)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(328, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-09-503-444A-21

  Query Match             99.3%;  Score 150;  DB 3;  Length 517;
  Best Local Similarity   99.3%;  Pred. No. 1.8e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              |||||||||||||||||||||||||| |||||
Db        303 CCTGGGGAAGAGCAGAGATATACGTACCAGG 333


RESULT 11
US-08-652-265-9
; Sequence 9, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
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;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(414, "a")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d7
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "g")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-9

  Query Match             99.3%;  Score 150;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.7e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
              ||||||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071


RESULT 12
US-08-652-265-10
; Sequence 10, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-10

  Query Match             99.3%;  Score 150;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.7e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db       1041 CCTGGGGAAGAGCAGAGATATACGTACCAGG 1071


RESULT 13
US-08-652-265-11
; Sequence 11, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-08-652-265-11

  Query Match             99.3%;  Score 150;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.7e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071


RESULT 14
US-08-652-265-12
; Sequence 12, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-12

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  Best Local Similarity   99.3%;  Pred. No. 2.7e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                ||||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTACCAGG 1071


RESULT 15
US-08-834-497A-9
; Sequence 9, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(414, "a")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d7
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "g")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-9

  Query Match             99.3%;  Score 150;  DB 3;  Length 1440;
  Best Local Similarity   99.3%;  Pred. No. 2.7e-43;
  Matches  150;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980

Qy         61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040

Qy        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                ||||||||||||||||||||||||| |||||
Db       1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071


Search completed: February 11, 2004, 19:17:05
Job time : 27.4222 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 14:16:30 ; Search time 1060.16 Seconds
(without alignments)
6052.274 Million cell updates/sec

Title: US-09-981-606-27_COPY_4652_4915
Perfect score: 264
Sequence: 1 gttcacactctctgcactac.....aaatcacaaccacagcaagg 264

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	264	100.0	560	9	AU279987	AU279987 AU279987
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	5	178.4	67.6	523	10	BF080089	BF080089 230846 MA
	6	178.4	67.6	550	12	BI339179	BI339179 364041 MA
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	9	176	66.7	481	10	BB851691	BB851691 BB851691
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	11	176	66.7	714	14	BY747346	BY747346 BY747346
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	13	176	66.7	1723	11	AK009581	AK009581 Mus muscu
	14	175	66.3	392	10	BF465475	BF465475 UI-M-CG0p
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	17	138.6	52.5	481	13	BQ561639	BQ561639 H4071E07-
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	19	136.8	51.8	407	13	BY159932	BY159932 BY159932
	20	123	46.6	364	13	BY202250	BY202250 BY202250
	21	121.4	46.0	351	13	BY319883	BY319883 BY319883
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	26	102.6	38.9	346	13	BY210730	BY210730 BY210730
	27	102.6	38.9	359	13	BY170353	BY170353 BY170353
	28	102	38.6	347	13	BY327323	BY327323 BY327323
	29	102	38.6	366	13	BY168570	BY168570 BY168570
	30	98.8	37.4	380	13	BY198206	BY198206 BY198206
	31	97.8	37.0	325	13	BY352115	BY352115 BY352115
	32	89	33.7	388	13	BY313216	BY313216 BY313216
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	35	56.2	21.3	867	9	AL547869	AL547869 AL547869
	36	55.6	21.1	629	14	CB154892	CB154892 K-EST0212
	37	55.2	20.9	289	14	H33644	H33644 EST109830 R
	38	54	20.5	757	13	BU940705	BU940705 AGENCOURT
	39	54	20.5	793	9	AU132916	AU132916 AU132916
	40	54	20.5	818	14	CB960984	CB960984 AGENCOURT
	41	54	20.5	868	9	AL550540	AL550540 AL550540
	42	54	20.5	886	14	CD244248	CD244248 AGENCOURT
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	44	54	20.5	934	13	BQ924251	BQ924251 AGENCOURT
	45	54	20.5	978	13	BX415555	BX415555 BX415555

ALIGNMENTS

RESULT 1
BM751283
LOCUS BM751283 544 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0027329 S9SNU601 Homo sapiens cDNA clone S9SNU601-12-G03 5', mRNA sequence.
ACCESSION BM751283
VERSION BM751283.1 GI:19080901
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 544)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 12 row: G column: 03
High quality sequence stop: 544.

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FEATURES             Location/Qualifiers
     source          1. .544
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /clone="S9SNU601-12-G03"
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                     /cell_type="Epithelial"
                     /cell_line="SNU-601"
                     /lab_host="Top10F'"
                     /clone_lib="S9SNU601"
                     /note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI;
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                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including SfiI
                     site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized with Superscript II using SfiI
                     oligo-dT primer. After first strand synthesis, RNA was
                     degraded by NaOH treatment and cDNA was amplified by PCR
                     reaction. The PCR products were digested with SfiI and
                     cloned into DraIII- digested pME18S-FL3 vector. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT      120 a    141 c    162 g    121 t
ORIGIN

  Query Match             100.0%;  Score 264;  DB 12;  Length 544;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-73;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        178 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 237

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Db        238 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 297

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db        298 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 357

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db        358 TGGAAAATCACAACCACAGCAAGG 381


RESULT 2
AU279987
LOCUS       AU279987                560 bp    mRNA    linear   EST 10-FEB-2003
DEFINITION  AU279987 CHONS2 Homo sapiens cDNA clone CHONS2002538 5', mRNA
            sequence.
ACCESSION   AU279987
VERSION     AU279987.1  GI:28299214
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 560)
  AUTHORS   Imabayashi,H., Gojo,S., Kiyono,T., Sugiyama,T., Irie,R., Isogai,T.,
            Mori,T., Hata,J., Tomoya,Y. and Umezawa,A.
  TITLE     Redifferentiation of dedifferentiated chondrocytes and
            chondrogenesis of human bone marrow stromal cells via chondrosphere
            formation with an expression profiling by large-scale cDNA analysis
  JOURNAL   Unpublished
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA Project, Sugiyama,T.; Wakamatsu,A.; Irie,R.; Umezawa
            ,A.; Fukuma,M.; Kusakari,S.; Hata,J.; Ishii,S.; Yamamoto,J.; Isono
            ,Y.; Saito,K.; Nakamura,Y.; Masuho,Y.; Nagai,K.; Isogai,T.
            HRI human cDNA project; cDNA library construction & 5'-end one
            pass sequencing: Helix Research Institute.
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                     /db_xref="taxon:9606"
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BASE COUNT      125 a    143 c    168 g    124 t
ORIGIN

  Query Match             100.0%;  Score 264;  DB 9;  Length 560;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-73;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        172 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 231

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Db        232 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 291

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db        292 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 351

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db        352 TGGAAAATCACAACCACAGCAAGG 375


RESULT 3
CB162561
LOCUS       CB162561                535 bp    mRNA    linear   EST 30-JAN-2003
DEFINITION  K-EST0223175 L17N670205n1 Homo sapiens cDNA clone
            L17N670205n1-27-D07 5', mRNA sequence.
ACCESSION   CB162561
VERSION     CB162561.1  GI:28148687
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
```

```
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 27  row: D  column: 07
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .535
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                     /clone="L17N670205n1-27-D07"
                     /sex="F"
                     /lab_host="Top10F'"
                     /clone_lib="L17N670205n1"
                     /note="Organism: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
                     Site_2: NotI; The library was contributed by the Soares
                     laboratory and it was constructed as described by Bonaldo,
                     M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
                     6(9): 791-806. RNA was prepared from harvested cell
                     culture."
BASE COUNT      113 a    140 c    161 g    121 t
ORIGIN

  Query Match           99.4%;  Score 262.4;  DB 14;  Length 535;
  Best Local Similarity  99.6%;  Pred. No. 2.1e-72;
  Matches  263;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 163

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 223

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 283

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 343

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||| ||||||||||||||||||
Db        344 TGGAATATCACAACCACAGCAAGG 367


RESULT 4
BF883952/c
LOCUS       BF883952                384 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  PM4-ET0209-151200-003-f07 ET0209 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF883952
VERSION     BF883952.1  GI:12274078
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM4&t2=PM4-ET0209-
            151200-003-f07&t3=2000-12-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 17
            High quality sequence stop: 384.
FEATURES             Location/Qualifiers
     source          1. .384
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="ET0209"
                     /note="Organism: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       92 a    112 c     87 g     93 t
ORIGIN

  Query Match           85.2%;  Score 225;  DB 10;  Length 384;
  Best Local Similarity  99.6%;  Pred. No. 1.4e-60;
  Matches  236;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         28 TGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATG 87
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATG 325

Qy         88 ACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGG 147
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 ACCAGCTG-TCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGG 266

Qy        148 TTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGG 207
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 TTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGG 206

Qy        208 ATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAGG 149


RESULT 5
BF080089
LOCUS       BF080089                523 bp    mRNA    linear   EST 18-OCT-2000
DEFINITION  230846 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BF080089
VERSION     BF080089.1  GI:10873919
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush
            ,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
```

```
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 48  row: E  column: 9
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .523
                      /organism="Sus scrofa"
                      /mol_type="mRNA"
                      /db_xref="taxon:9823"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /clone_lib="MARC 2PIG"
                      /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                      Library made from pooled tissue from testis, ovary,
                      endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      103 a    175 c    152 g     93 t
ORIGIN

  Query Match             67.6%;  Score 178.4;  DB 10;  Length 523;
  Best Local Similarity   80.4%;  Pred. No. 1.1e-45;
  Matches  209;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          4 CACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGT 63
              ||||||| |||| || ||||||||||||| ||||| |||| || || || ||  || |||
Db        182 CACACTCCCTGCTCTTCCTCTTCATGGGCGCCTCGGAGCCAGATCTCGGGCTGCCCCTGT 241

Qy         64 TTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCC 123
              |||| || |||||||||||||||| |||||||||| |||| ||| |||| ||||||||||
Db        242 TTGAGGCCTTGGGCTACGTGGACGACCAGCTGTTTGTGTCCTACAATCACGAGAGTCGCC 301

Qy        124 GTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGC 183
              |||  ||||| ||  | || ||| | ||  |||     || | |||  ||||||||||||
Db        302 GTGCAGAGCCTCGCGCCCCCTGGCTCTCGGGTAAGGCCTCCAACCAACTGTGGCTGCAGC 361

Qy        184 TGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGG 243
              | || ||||| |||||||||||||||||||||||||| || ||||||||||| || ||||
Db        362 TAAGCCAGAGCCTGAAAGGGTGGGATCACATGTTCACCGTGGACTTCTGGACCATCATGG 421

Qy        244 AAAATCACAACCACAGCAAG 263
              | || |||||| ||||||||
Db        422 ACAACCACAACTACAGCAAG 441


RESULT 6
BI339179
LOCUS       BI339179                 550 bp    mRNA    linear   EST 30-JUL-2001
DEFINITION  364041 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI339179
VERSION     BI339179.1  GI:15032462
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush
            ,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 100  row: C  column: 24
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .550
                      /organism="Sus scrofa"
                      /mol_type="mRNA"
                      /db_xref="taxon:9823"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /clone_lib="MARC 2PIG"
                      /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                      Library made from pooled tissue from testis, ovary,
                      endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      108 a    180 c    164 g     98 t
ORIGIN

  Query Match             67.6%;  Score 178.4;  DB 12;  Length 550;
  Best Local Similarity   80.4%;  Pred. No. 1.2e-45;
  Matches  209;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          4 CACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGT 63
              ||||||| |||| || ||||||||||| ||||| |||| || || || ||  || |||
Db        155 CACACTCCCTGCTCTTCCTCTTCATGGGCGCCTCGGAGCCAGATCTCGGGCTGCCCCTGT 214

Qy         64 TTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCC 123
              |||| || |||||||||||||||| |||||||||| |||| ||| |||| ||||||||||
Db        215 TTGAGGCCTTGGGCTACGTGGACGACCAGCTGTTTGTGTCCTACAATCACGAGAGTCGCC 274

Qy        124 GTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGC 183
              |||  ||||| ||  | || ||| | ||  |||     || | |||  ||||||||||||
Db        275 GTGCAGAGCCTCGCGCCCCCTGGCTCTCGGGTAAGGCCTCCAACCAACTGTGGCTGCAGC 334

Qy        184 TGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGG 243
              | || ||||| |||||||||||||||||||||||| || ||||||||||| || ||||
Db        335 TAAGCCAGAGCCTGAAAGGGTGGGATCACATGTTCACCGTGGACTTCTGGACCATCATGG 394

Qy        244 AAAATCACAACCACAGCAAG 263
              | || |||||| ||||||||
Db        395 ACAACCACAACTACAGCAAG 414


RESULT 7
BG747345
LOCUS       BG747345                 819 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602704818F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857941 5',
            mRNA sequence.
ACCESSION   BG747345
VERSION     BG747345.1  GI:14057998
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: NIH Intramural Sequencing Center
            Clone distribution: MGC clone distribution information can be
```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1711 row: d column: 06
High quality sequence stop: 792.

FEATURES Location/Qualifiers
source 1. .819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4857941"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 202 a 201 c 235 g 181 t
ORIGIN

Query Match 67.4%; Score 178; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         87 GACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGG 146
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGG 60

Qy        147 GTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGG 206
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGG 120

Qy        207 GATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAGG 264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAGG 178
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RESULT 8
AA217236/c
LOCUS AA217236 464 bp mRNA linear EST 06-FEB-1997
DEFINITION mu89b05.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone IMAGE:652689 5' similar to TR:G940354 G940354 CLASS I HISTOCOMPATIBILITY ANTIGEN-LIKE PROTEIN. ;, mRNA sequence.
ACCESSION AA217236
VERSION AA217236.1 GI:1826237
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 464)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:398537
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham.

FEATURES Location/Qualifiers
source 1. .464
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:652689"
/sex="male"
/tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mouse lymph node NbMLN"
/note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGATACTTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 101 a 136 c 119 g 108 t
ORIGIN

Query Match 66.7%; Score 176; DB 9; Length 464;
Best Local Similarity 79.2%; Pred. No. 6.2e-45;
Matches 209; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

```
Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||| |||||     ||||||||||||||||||||||  ||||| || ||  | |
Db        449 GTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTGCCTT 390

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||| |||  |||||| ||||||||||||||| || |||| |||  ||||||||||||
Db        389 TGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAGAGTC 330

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||  ||||||  |  | || ||| | |        ||  |||||||||  |||||||||
Db        329 GCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGGCTGC 270

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              | |||||||||| ||||||||||||||  ||||||||  || ||||||||||| || |
Db        269 ATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACCATCA 210

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              |||  ||  | ||||||||  ||||
Db        209 TGGGCAACTATAACCACAGTAAGG 186
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RESULT 9
BB851691
LOCUS BB851691 481 bp mRNA linear EST 26-NOV-2001
DEFINITION BB851691 RIKEN full-length enriched, B16 F10Y cells Mus musculus cDNA clone G370002P09 5', mRNA sequence.
ACCESSION BB851691
VERSION BB851691.1 GI:17093145
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 481)
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.

```
            2001)
  JOURNAL   Unpublished
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .481
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G370002P09"
                     /cell_type="B16 F10Y cells"
                     /clone_lib="RIKEN full-length enriched, B16 F10Y cells"
BASE COUNT       95 a    134 c    140 g    112 t
ORIGIN

  Query Match           66.7%;  Score 176;  DB 10;  Length 481;
  Best Local Similarity   79.2%;  Pred. No. 6.3e-45;
  Matches  209;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||| |||||    |||||||||||||||||||||||||  ||||| || ||  | |
Db        186 GTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTGCCTT 245

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||| |||  |||||| |||||||||||||| || |||| |||  ||||||||||||
Db        246 TGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAGAGTC 305

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||  ||||||  |  | || ||| | |        ||  |||||||| |||||||||
Db        306 GCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGGCTGC 365

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              | ||||||||||| |||||||||||||  |||||||||  || ||||||||||| || | |
Db        366 ATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACCATCA 425

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              |||  ||  | ||||||| ||||
Db        426 TGGGCAACTATAACCACAGTAAGG 449


RESULT 10
BE994943
LOCUS       BE994943                489 bp    mRNA    linear   EST 29-APR-2002
DEFINITION  UI-M-CG0p-bik-d-03-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
            UI-M-CG0p-bik-d-03-0-UI 3', mRNA sequence.
ACCESSION   BE994943
VERSION     BE994943.1  GI:10678689
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
            clones from RESEARCH GENETICS. It should be noted that Bento Soares
            is generating a small number of additional specialized
            non-redundant arrays of BMAP cDNAs whose availability will be
            considered under appropriate and limited collaborative arrangements
            The tissue for this library was contributed by Dr. Xin-Yuan Fu,
            Yale University School of Medicine The following repetitive
            elements were found in this cDNA sequence: 1-31, >(CAG
            )n#Simple_repeat
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .489
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-CG0p-bik-d-03-0-UI"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NIH_BMAP_Ret4_S2"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_Ret4_S2 library is a subtracted library,
                     ultimately derived from mouse retina tissue libraries at
                     various stages of development. For a detailed description
                     of the library from which this clone was derived, please
                     visit our web site at brainest.eng.uiowa.edu. The tissue
                     for this library was contributed by Dr. Xin-Yuan Fu, Yale
                     University School of Medicine
                     TAG_SEQ=None found"
BASE COUNT      103 a    133 c    144 g    109 t
ORIGIN

  Query Match           66.7%;  Score 176;  DB 10;  Length 489;
  Best Local Similarity   79.2%;  Pred. No. 6.4e-45;
  Matches  209;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||| |||||    |||||||||||||||||||||||||  ||||| || ||  | |
Db         63 GTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTGCCTT 122

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||| |||  |||||| |||||||||||||| || |||| |||  ||||||||||||
Db        123 TGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAGAGTC 182

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||  ||||||  |  | || ||| | |        ||  |||||||| |||||||||
Db        183 GCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGGCTGC 242

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
```

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                |||||||||||| |||||||||||||| |||||||||  || ||||||||||| || |
Db        243 ATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACCATCA 302

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              |||  ||  | |||||||| ||||
Db        303 TGGGCAACTATAACCACAGTAAGG 326


RESULT 11
BY747346
LOCUS       BY747346                714 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY747346 RIKEN full-length enriched, 2 days neonate thymus thymic
            cells (NOD) Mus musculus cDNA clone E430034J19 5', mRNA sequence.
ACCESSION   BY747346
VERSION     BY747346.1  GI:27175512
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 714)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.
            , Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
            Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
            Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
            Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
            ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
            ,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.
            , Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
            Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
            King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
            ,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki
            ,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
            Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
            Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring
            ,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou
            ,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale
            ,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y.,
            Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa
            ,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
            Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura
            ,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.
            , Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii
            ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
            ,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
            ,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
            ,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
            Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
            ,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
            Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
            Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
            Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
            Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .714
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="NOD"
                      /db_xref="taxon:10090"
                      /clone="E430034J19"
                      /tissue_type="thymus"
                      /cell_type="thymic cells"
                      /clone_lib="RIKEN full-length enriched, 2 days neonate
                      thymus thymic cells (NOD)"
BASE COUNT      166 a    194 c    208 g    146 t
ORIGIN

  Query Match           66.7%;  Score 176;  DB 14;  Length 714;
  Best Local Similarity   79.2%;  Pred. No. 7.7e-45;
  Matches  209;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              |||||| |||||    |||||||||||||||||||||||||  ||||| || ||  | |
Db        182 GTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTGCCTT 241

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        242 TGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAGAGTC 301

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              |||||| |||||| |  | || ||| | |        ||  ||||||||| |||||||||
Db        302 GCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGGCTGC 361

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db        362 ATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACCATCA 421

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              |||  ||  | |||||||| ||||
Db        422 TGGGCAACTATAACCACAGTAAGG 445


RESULT 12
AK088986
LOCUS       AK088986                1719 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN
            full-length enriched library, clone:E430034J19
            product:hemochromatosis, full insert sequence.
ACCESSION   AK088986
VERSION     AK088986.1  GI:26354115
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
```

JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1719)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
source 1. .1719
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/strain="NOD"
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/db_xref="taxon:10090"
/clone="E430034J19"
/cell_type="thymic cells"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="2 days neonate"
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PKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLELGRGVLGQQVP
TLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVLPNGDETYQ
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polyA_signal 1690. .1695
/note="putative"
polyA_site 1719
/note="putative"

BASE COUNT 405 a 452 c 455 g 407 t
ORIGIN

Query Match 66.7%; Score 176; DB 11; Length 1719;
Best Local Similarity 79.2%; Pred. No. 1.2e-44;
Matches 209; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||| |||||    |||||||||||||||||||||||||  ||||| || ||  | |
Db        182 GTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTGCCTT 241

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||| |||   |||||| |||||||||||||||| || |||| |||  ||||||||||
Db        242 TGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAGAGTC 301

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||  |||||| | | || ||| | |    ||  ||||||||| |||||||||
Db        302 GCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGGCTGC 361

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              | |||||||||||| |||||||||||||  |||||||||  || ||||||||||| || |
Db        362 ATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACCATCA 421

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              |||  ||  | ||||||||| ||||
Db        422 TGGGCAACTATAACCACAGTAAGG 445
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RESULT 13

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AK009581
LOCUS       AK009581                1723 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
            library, clone:2310032M04 product:hemochromatosis, full insert
            sequence.
ACCESSION   AK009581
VERSION     AK009581.1  GI:12844462
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1723)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
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Matches 209; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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ACCESSION BF465475
VERSION BF465475.1 GI:11534658
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 392)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 1-31, >(CAG)n#Simple_repeat
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TAG_SEQ=None found"
BASE COUNT 74 a 107 c 115 g 93 t 3 others
ORIGIN

Query Match 66.3%; Score 175; DB 10; Length 392;
Best Local Similarity 78.8%; Pred. No. 1.2e-44;
Matches 208; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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RESULT 15
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DEFINITION BY745026 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830071K08 5', mRNA sequence.
ACCESSION BY745026
VERSION BY745026.1 GI:27171997
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 668)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda ,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno ,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
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BASE COUNT 138 a 177 c 200 g 148 t 5 others
ORIGIN

Query Match 66.3%; Score 175; DB 14; Length 668;
Best Local Similarity 78.8%; Pred. No. 1.5e-44;
Matches 208; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Scoring table: IDENTITY_NUC
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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	264	100.0	1317	24	ABK49917	DNA encoding beta
	2	264	100.0	1440	18	AAT96691	Hereditary haemoch
	3	264	100.0	1440	22	AAC68429	Human hereditary h
	4	264	100.0	1440	22	AAC68430	Human hereditary h
	5	264	100.0	2506	21	AAA96769	cDNA sequence enco
	6	264	100.0	2727	19	AAV23525	Haemochromatosis g
	7	264	100.0	5982	25	ABV93934	Human colon specif
	8	264	100.0	10825	18	AAT96690	Hereditary haemoch
	9	264	100.0	10825	22	AAC68425	Human hereditary h
	10	264	100.0	10825	22	AAC68426	Human hereditary h
	11	264	100.0	12146	21	AAA96794	Genomic DNA of a h
c	12	264	100.0	235033	19	AAV57926	Hereditary haemoch
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	15	262.4	99.4	1440	22	AAC68432	Human hereditary h
	16	262.4	99.4	10825	22	AAC68427	Human hereditary h
	17	262.4	99.4	10825	22	AAC68428	Human hereditary h
	18	251.6	95.3	596	22	AAI63897	Human polynucleoti
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c	22	74.4	28.2	76	22	AAF58232	Oligonucleotide D1
c	23	70	26.5	75	22	AAF58246	Oligonucleotide D1
c	24	68.4	25.9	75	22	AAF58247	Oligonucleotide D1
	25	55.2	20.9	575	22	AAI63896	Human polynucleoti
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	31	45	17.0	45	21	AAA12669	Probe used for gen
	32	43.8	16.6	1112	21	AAA48668	cDNA encoding chic
	33	43.6	16.5	1032	20	AAX89245	MHC class I antige
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	37	41.6	15.8	12930	25	ABZ74995	Human MHC class I
	38	41.2	15.6	261	24	ABK88254	YF-VI DNA sequence
	39	41.2	15.6	261	24	AAD29186	Chicken MHc class
	40	40.6	15.4	264	24	AAD29183	Chicken MHc class
	41	40.6	15.4	3324	20	AAX60262	Nucleic acid seque
	42	40.4	15.3	313	21	AAC08552	Human secreted pro
	43	40	15.2	40	22	AAC68459	Sequence surroundi
	44	40	15.2	148834	24	ABK83570	Human cDNA differe
	45	39.8	15.1	720	24	ABK87873	Mouse dep.3 mutant

ALIGNMENTS

RESULT 1
ABK49917
ID ABK49917 standard; cDNA; 1317 BP.
XX
AC ABK49917;
XX
DT 15-JUL-2002 (first entry)
XX
DE DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
XX
KW Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
KW iron absorption regulator; intracellular iron absorption; lung injury;
KW haemochromatosis; transfusion; thalassaemia; haemolytic anaemia;
KW chronic infection; transferrin receptor; TfR; brain tumour; cancer;
KW oxidative stress disorder; tissue damage; vascular disease;
KW inflammation; atherosclerosis; autoimmune disease;
KW inflammatory condition; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1317
FT /*tag= a
FT /product= "beta2M/HFE monochain"
XX
PN WO200224929-A2.
XX
PD 28-MAR-2002.
XX
PF 24-SEP-2001; 2001WO-US29873.
XX

PR 22-SEP-2000; 2000US-234843P.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (MCIN/) MCINNIS P.
XX
PI Ehrlich R, Rotem-Yehudar R, Laham N;
XX
DR WPI; 2002-383192/41.
DR P-PSDB; AAU80035.
XX
PT Soluble beta 2 microglobulin/HFE monochain useful for treating
PT iron-overload conditions e.g. thalassemia and chronic infections,
PT comprises human beta 2 microglobulin linked to alpha domains of HFE by
PT a linker peptide -
XX
PS Example 2; Fig 2; 77pp; English.
XX
CC The invention relates to a soluble polypeptide (I) of beta 2
CC microglobulin (beta2m)/HFE monochain comprising human beta2m (or its
CC analogue or active fragment), linked to alpha1-alpha3 domains of human
CC HFE (a central regulator of iron absorption; undefined), or its analogue
CC or active fragment, by a flexible linker peptide, or a functional
CC derivative or salt of (I). (I) is useful for reducing intracellular iron
CC absorption in patients having hereditary haemochromatosis, transfusions,
CC thalassaemias, haemolytic anaemia or chronic infections, and for
CC delivering a therapeutic to cells that over-express transferrin receptor
CC (TfR) which are preferably lymphocytes or leukocytes, across the blood-
CC brain barrier. (I) is further useful for treating brain tumour. (I)
CC is also useful for treating oxidative stress disorders resulting in
CC tissue damage e.g. vascular diseases, inflammation, atherosclerosis,
CC lung injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful
CC as a platform for drug delivery of therapeutic use for cancer,
CC autoimmune diseases and inflammatory conditions. The monochain manifests
CC specific characteristics advantageous for drug delivery systems. It is a
CC soluble, stable and fully conformed protein. It binds specifically to
CC transferrin receptor (TfR) and therefore targets cells that over-express
CC this receptor. It is continuously internalised by the target cells, thus
CC enabling efficient drug delivery. It dissociates from the receptor in the
CC cells, minimising side effects. It negatively regulates iron absorption,
CC reducing growth of undesired cells and preventing lymphocyte activation.
CC It is not diluted in the blood as is transferrin. It should not induce an
CC immune response since it is a self non-polymeric protein and delivery of
CC drugs via monochain is expected to overcome drug-resistance since it is a
CC natural TfR-binding protein. The present sequence represents the
CC coding sequence of beta2m/HFE monochain.
XX
SQ Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;

Query Match 100.0%; Score 264; DB 24; Length 1317;
Best Local Similarity 100.0%; Pred. No. 9.2e-77;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 472

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 532

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 592

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 652

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db        653 TGGAAAATCACAACCACAGCAAGG 676
```

RESULT 2
AAT96691
ID AAT96691 standard; cDNA; 1440 BP.
XX
AC AAT96691;
XX
DT 14-APR-1998 (first entry)
XX
DE Hereditary haemochromatosis gene cDNA clone.
XX
KW Hereditary haemochromatosis; metal toxicity; diagnosis;
KW gene therapy; prenatal screening; human; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	222.1268
FT		/*tag= a
FT	mutation	408
FT		/*tag= g
FT		/note= "C to G substitution (24d2 mutation)
FT		results in His to Asp substitution"
FT	variation	414
FT		/*tag= h
FT		/note= "A to T substitution (24d7 variant)
FT		results in Ser to Cys substitution"
FT	mutation	1066
FT		/*tag= i
FT		/note= "G to A substitution (24d1 mutation
FT		associated with HH), results in Cys to
FT		Tyr substitution"

XX
PN WO9738137-A1.
XX
PD 16-OCT-1997.
XX
PF 04-APR-1997; 97WO-US06254.
XX
PR 23-MAY-1996; 96US-0652265.
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
XX
PA (MERC-) MERCATOR GENETICS INC.
XX
PI Drayna DT, Feder JN, Gnirke A, Ruddy D, Thomas WJ;
PI Tsuchihashi Z, Wolff RK;
XX
DR WPI; 1997-512743/47.
DR P-PSDB; AAW36499.
XX
PT Hereditary haemochromatosis gene and variants - useful for diagnosis
PT and treatment of hereditary haemochromatosis disease
XX
PS Disclosure; Fig 4; 115pp; English.
XX
CC This cDNA clone, designated cDNA24, is derived from human gene
CC whose mutated form is associated with hereditary haemochromatosis
CC (HH). It was obtained from a directionally cloned plasmid-based
CC cDNA library following identification of the HH locus in the HLA
CC region of chromosome 6. A single mutation (24d1) in the HH gene
CC appears responsible for the majority of HH disease. This comprises
CC a G to A substitution that is present in 86% of affected
CC chromosomes and in 4% of unaffected chromosomes. It results in a
CC Cys to Tyr substitution in the encoded protein (see AAW36499) at a
CC critical disulphide bridge important for secondary structure. The
CC following are claimed: a 10825 bp genomic DNA sequence (I) (see
CC AAT96690), the 1437 bp cDNA sequence (Ia) and their 24d1, 24d2 and
CC 24d7 variants; a cloning or expression vector; host cells; a
CC peptide product chosen from the HH gene product, its variants
CC (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC residues of these; an antibody produced using the peptide; a method
CC to determine the presence or absence of the common HH gene
CC mutation; an animal model for the HH disease; metal chelation

CC agents, T-cell differentiation factors and therapeutic agents for
CC the mitigation of injury due to oxidative process in vivo or
CC mitigation of iron overload; a method for screening potential
CC therapeutic agents for activity in connection with HH disease; an
CC antisense oligonucleotide directed against a transcriptional
CC product of a nucleic acid sequence as above; and oligonucleotides
CC or pairs of oligonucleotides covering a range of nucleotides from
CC (I), (Ia) or their variants, useful for detecting a polymorphism in
CC the HH gene. The invention also relates to methods for screening
CC for HH homozygotes, to HH diagnosis, prenatal screening and
CC diagnosis, and therapies of HH disease, including gene therapy,
CC protein- and antibody-based therapeutics, and small molecule
CC therapeutics.
XX
SQ Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

Query Match 100.0%; Score 264; DB 18; Length 1440;
Best Local Similarity 100.0%; Pred. No. 9.6e-77;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 417

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 477

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db        538 TGGAAAATCACAACCACAGCAAGG 561
```

RESULT 3
AAC68429
ID AAC68429 standard; DNA; 1440 BP.
XX
AC AAC68429;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis cDNA.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ss.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 4; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

Query Match 100.0%; Score 264; DB 22; Length 1440;
Best Local Similarity 100.0%; Pred. No. 9.6e-77;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db        298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 417

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 477

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db        538 TGGAAAATCACAACCACAGCAAGG 561
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RESULT 4
AAC68430
ID AAC68430 standard; DNA; 1440 BP.
XX
AC AAC68430;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis 24d1 mutation cDNA.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ss.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful

```
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;

  Query Match           100.0%;  Score 264;  DB 22;  Length 1440;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-77;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 417

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 477

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db        538 TGGAAAATCACAACCACAGCAAGG 561


RESULT 5
AAA96769
ID   AAA96769 standard; cDNA; 2506 BP.
XX
AC   AAA96769;
XX
DT   19-FEB-2001  (first entry)
XX
DE   cDNA sequence encoding a histocompatibility iron loading (HFE) protein.
XX
KW   Human; histocompatibility iron loading protein; HFE protein;
KW   major histocompatibility complex; non-classical class I gene;
KW   chromosome 6p; iron disorder; haemochromatosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1044
FT                   /*tag=  a
FT                   /product= "histocompatibility iron loading (HFE) protein"
FT   sig_peptide     1..66
FT                   /*tag=  b
FT   mutation        187
FT                   /*tag=  c
FT                   /note= "if this base is mutated to G, then the
FT                          protein contains the mutation H63D"
FT   mutation        193
FT                   /*tag=  d
FT                   /note= "if this base is mutated to T, then the
FT                          protein contains the mutation S65C"
FT   mutation        277
FT                   /*tag=  e
FT                   /note= "if this base is mutated to C, then the
FT                          protein contains the mutation G93R"
FT   mutation        314
FT                   /*tag=  f
FT                   /note= "if this base is mutated to C, then the
FT                          protein contains the mutation I105T, which
FT                          is associated with an iron overload disorder"
XX
PN   WO200058515-A1.
XX
PD   05-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US07982.
XX
PR   26-MAR-1999;   99US-0277457.
XX
PA   (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI   Rothenberg BE,  Sawada-Hirai R,  Barton JC;
XX
DR   WPI; 2000-647244/62.
DR   P-PSDB; AAB19149.
XX
PT   Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT   susceptibility to develop it, by determining the presence of a mutation
PT   in exon 2 or an intron of a histocompatibility iron loading nucleic
PT   acid -
XX
PS   Disclosure; Page 2-3; 55pp; English.
XX
CC   The present sequence encodes a human histocompatibility iron loading
CC   (HFE) protein. The HFE gene is a major histocompatibility (MHC)
CC   non-classical class I gene located on chromosome 6p. Mutations in the
CC   gene lead to iron disorders. The specification describes a method for
CC   diagnosing an iron disorder or a genetic susceptibility to develop the
CC   disorder in a mammal. The method comprises determining the presence of
CC   a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
CC   is not a C to G missense mutation at nucleotide 187 of the sequence
CC   given in A96769 (Genbank Accession number U60319). The presence of the
CC   mutation indicates the disorder or the genetic susceptibility to the
CC   disorder. The method is used to diagnose an iron disorder
CC   e.g. haemochromatosis, or a genetic susceptibility to develop it.
XX
SQ   Sequence 2506 BP; 648 A; 552 C; 596 G; 710 T; 0 other;

  Query Match           100.0%;  Score 264;  DB 21;  Length 2506;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-76;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 136

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 196

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 256

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 316

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db        317 TGGAAAATCACAACCACAGCAAGG 340


RESULT 6
AAV23525
ID   AAV23525 standard; mRNA; 2727 BP.
XX
AC   AAV23525;
```

XX
DT 10-JUL-1998 (first entry)
XX
DE Haemochromatosis gene.
XX
KW Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
KW autosomal recessive disorder; ss.
XX
OS Homo sapiens.
XX
PN WO9807884-A1.
XX
PD 26-FEB-1998.
XX
PF 22-AUG-1997; 97WO-AU00539.
XX
PR 03-SEP-1996; 96AU-0002083.
PR 23-AUG-1996; 96AU-0001849.
XX
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Busfield F, Cullen LM, Jazwinska EC, Powell LW;
XX
DR WPI; 1998-179064/16.
XX
PT Detection of autosomal recessive disorder - particularly hereditary
PT haemochromatosis, by detecting a mutation in the HC gene
XX
PS Disclosure; Page -; 32pp; English.
XX
CC This sequence represents the haemochromatosis (HC) gene. Mutations in
CC this sequence are detected using the method of the invention. The method
CC is for identifying an individual with hereditary haemochromatosis (HH) or
CC a predisposition to develop HH or to genetically pass on HH to an
CC offspring, comprising isolating a biological sample and amplifying a
CC region of genomic DNA in the biological sample encompassing all or part
CC of the DNA between markers D6S265 and D6S276, and detecting at least one
CC homozygous or heterozygous mutation in a nucleotide within the region.
CC The method can also be used for identifying an individual with an
CC autosomal recessive disorder (ARD) or predisposition to develop and/or
CC genetically pass on an ARD to an offspring, comprises isolating a
CC biological sample from the individual and screening genomic DNA in the
CC sample for the presence of a homozygous or heterozygous mutation in a
CC gene, the normal function of which, is required to prevent progression of
CC the disorder. The method(s) can be used to identify individuals that are
CC homozygous or heterozygous (carriers) for the mutation causing the ARD.
CC Especially the method is used to diagnose HH or predisposition to HH by
CC detecting a Cys282Tyr substitution. Individuals homozygous for this
CC mutation have HH and heterozygotes are potential carriers of the
CC disease.
XX
SQ Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;

Query Match 100.0%; Score 264; DB 19; Length 2727;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 417

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 477

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537
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```
Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db        538 TGGAAAATCACAACCACAGCAAGG 561
```

RESULT 7
ABV93934
ID ABV93934 standard; DNA; 5982 BP.
XX
AC ABV93934;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human colon specific nucleic acid, SEQ ID 25.
XX
KW Human; colon; cytostatic; vaccine; gene therapy; colon cancer;
KW colon disorder; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200277234-A2.
XX
PD 03-OCT-2002.
XX
PF 31-OCT-2001; 2001WO-US48414.
XX
PR 31-OCT-2000; 2000US-244758P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Sun Y, Recipon H, Ghosh MG, Liu C;
XX
DR WPI; 2003-018928/01.
XX
PT New isolated colon-specific nucleic acid molecule, useful for treating
PT colon cancer, and diagnosing or monitoring the presence of metastases
PT of colon cancer in a patient -
XX
PS Claim 1; Page 155-156; 216pp; English.
XX
CC The present invention relates to human colon specific nucleic acids
CC (ABV93910-ABV94009) and proteins (ABP68360-ABP68435). The nucleic acids
CC and proteins are useful for treating colon cancer and colon disorders,
CC and diagnosing or monitoring the presence of colon disorders and
CC metastases of colon cancer in a patient.
XX
SQ Sequence 5982 BP; 1659 A; 1247 C; 1518 G; 1556 T; 2 other;

Query Match 100.0%; Score 264; DB 25; Length 5982;
Best Local Similarity 100.0%; Pred. No. 1.7e-76;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3402 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3461

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3462 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3521

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3522 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3581

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3582 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 3641

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       3642 TGGAAAATCACAACCACAGCAAGG 3665
```

```
RESULT 8
AAT96690
ID   AAT96690 standard; DNA; 10825 BP.
XX
AC   AAT96690;
XX
DT   14-APR-1998  (first entry)
XX
DE   Hereditary haemochromatosis gene.
XX
KW   Hereditary haemochromatosis; metal toxicity; diagnosis;
KW   gene therapy; prenatal screening; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "contains introns"
FT   intron          437..3761
FT                   /*tag=  b
FT                   /number= 1
FT   intron          4026..4234
FT                   /*tag=  c
FT                   /number= 2
FT   intron          4511..5605
FT                   /*tag=  d
FT                   /number= 3
FT   intron          5882..6039
FT                   /*tag=  e
FT                   /number= 4
FT   intron          6154..7106
FT                   /*tag=  f
FT                   /number= 5
FT   mutation        3872
FT                   /*tag=  g
FT                   /note= "C to G substitution (24d2 mutation)
FT                          results in His to Asp substitution"
FT   variation       3878
FT                   /*tag=  h
FT                   /note= "A to T substitution (24d7 variant)
FT                          results in Ser to Cys substitution"
FT   mutation        5834
FT                   /*tag=  i
FT                   /note= "G to A substitution (24d1 mutation
FT                          associated with HH), results in Cys to
FT                          Tyr substitution"
XX
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US06254.
XX
PR   23-MAY-1996;   96US-0652265.
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   P-PSDB; AAW36499.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis
PT   and treatment of hereditary haemochromatosis disease
XX
PS   Disclosure; Fig 3; 115pp; English.
XX
CC   This genomic DNA sequence corresponds to the human gene whose
CC   mutated form is associated with hereditary haemochromatosis (HH).
CC   To identify this novel gene, allelic association patterns were
CC   determined between known markers and the HH locus in the HLA region
CC   of chromosome 6.  A physical clone coverage was then generated
CC   extending from D6S265, which is a marker that is centromeric of
CC   HLA-A, in a telomeric direction through D6S276, a marker at which
CC   the allelic association was no longer observed.  A single mutation
CC   (24d1) in the HH gene appears responsible for the majority of HH
CC   disease.  This comprises a G to A substitution that is present in
CC   86% of affected chromosomes and in 4% of unaffected chromosomes.
CC   It results in a Cys to Tyr substitution in the encoded protein (see
CC   AAW36499) at a critical disulphide bridge important for secondary
CC   structure.  The following are claimed: the HH genomic DNA (I), a
CC   1437 bp cDNA sequence (Ia) (see AAT96691) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a
CC   peptide product chosen from the HH gene product, its variants
CC   (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC   residues of these; an antibody produced using the peptide; a method
CC   to determine the presence or absence of the common HH gene
CC   mutation; an animal model for the HH disease; metal chelation
CC   agents, T-cell differentiation factors and therapeutic agents for
CC   the mitigation of injury due to oxidative process in vivo or
CC   mitigation of iron overload; a method for screening potential
CC   therapeutic agents for activity in connection with HH disease; an
CC   antisense oligonucleotide directed against a transcriptional
CC   product of a nucleic acid sequence as above; and oligonucleotides
CC   or pairs of oligonucleotides covering a range of nucleotides from
CC   (I), (Ia) or their variants, useful for detecting a polymorphism in
CC   the HH gene.  The invention also relates to methods for screening
CC   for HH homozygotes, to HH diagnosis, prenatal screening and
CC   diagnosis, and therapies of HH disease, including gene therapy,
CC   protein- and antibody-based therapeutics, and small molecule
CC   therapeutics.
XX
SQ   Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;

  Query Match             100.0%;  Score 264;  DB 18;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-76;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAGG 4025


RESULT 9
AAC68425
ID   AAC68425 standard; DNA; 10825 BP.
XX
AC   AAC68425;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
```

OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
DR P-PSDB; AAB36869.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;

Query Match 100.0%; Score 264; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 2.2e-76;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAGG 4025
```

RESULT 10
AAC68426
ID AAC68426 standard; DNA; 10825 BP.
XX
AC AAC68426;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis 24d1 mutation DNA.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ds.
XX

OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
DR P-PSDB; AAB36870.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;

Query Match 100.0%; Score 264; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 2.2e-76;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAGG 4025
```

RESULT 11
AAA96794
ID AAA96794 standard; cDNA; 12146 BP.
XX
AC AAA96794;
XX
DT 19-FEB-2001 (first entry)
XX
DE Genomic DNA of a histocompatibility iron loading (HFE) gene.
XX
KW Human; histocompatibility iron loading protein; HFE protein;
KW major histocompatibility complex; non-classical class I gene;
KW chromosome 6p; iron disorder; haemochromatosis; ss.

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1028..1324
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FT                   /number= 1
FT   intron          1325..4651
FT                   /*tag= b
FT                   /number= 1
FT   exon            4652..4915
FT                   /*tag= c
FT                   /number= 2
FT   intron          4916..5124
FT                   /*tag= d
FT                   /number= 2
FT   exon            5125..5400
FT                   /*tag= e
FT                   /number= 3
FT   intron          5401..6493
FT                   /*tag= f
FT                   /number= 3
FT   exon            6494..6769
FT                   /*tag= g
FT                   /number= 4
FT   intron          6770..6927
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FT                   /number= 4
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FT                   /number= 5
FT   intron          7042..7994
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FT                   /*tag= l
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FT   exon            10206..10637
FT                   /*tag= m
XX
PN   WO200058515-A1.
XX
PD   05-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US07982.
XX
PR   26-MAR-1999;   99US-0277457.
XX
PA   (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI   Rothenberg BE,  Sawada-Hirai R,  Barton JC;
XX
DR   WPI; 2000-647244/62.
XX
PT   Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT   susceptibility to develop it, by determining the presence of a mutation
PT   in exon 2 or an intron of a histocompatibility iron loading nucleic
PT   acid -
XX
PS   Example 1; Page 21-28; 55pp; English.
XX
CC   The present sequence represents the human histocompatibility iron
CC   loading (HFE) gene. The HFE gene is a major histocompatibility (MHC)
CC   non-classical class I gene located on chromosome 6p. Mutations in the
CC   gene lead to iron disorders. The specification describes a method for
CC   diagnosing an iron disorder or a genetic susceptibility to develop the
CC   disorder in a mammal. The method comprises determining the presence of
CC   a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
CC   is not a C to G missense mutation at nucleotide 187 of the sequence
CC   given in A96769 (Genbank Accession number U60319). The presence of the
CC   mutation indicates the disorder or the genetic susceptibility to the
CC   disorder. The method is used to diagnose an iron disorder
CC   e.g. haemochromatosis, or a genetic susceptibility to develop it.
XX
SQ   Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 other;

  Query Match            100.0%;  Score 264;  DB 21;  Length 12146;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-76;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4652 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 4711

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4712 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 4771

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4772 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 4831

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4832 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4891

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       4892 TGGAAAATCACAACCACAGCAAGG 4915


RESULT 12
AAV57926/c
ID   AAV57926 standard; DNA; 235033 BP.
XX
AC   AAV57926;
XX
DT   23-DEC-1998  (first entry)
XX
DE   Hereditary haemochromatosis subregion from an unaffected individual.
XX
KW   Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW   diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW   BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW   type 1 sodium transport gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO9814466-A1.
XX
PD   09-APR-1998.
XX
PF   30-SEP-1997;   97WO-US17658.
XX
PR   07-MAY-1997;   97US-0852495.
PR   01-OCT-1996;   96US-0724394.
XX
PA   (PROG-) PROGENTIOR INC.
XX
PI   Feder JN,  Kronmal GS,  Lauer PM,  Ruddy DA,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1998-240014/21.
XX
PT   Hereditary haemochromatosis gene products - used to develop products
PT   for the diagnosis and treatment of hereditary disorders in iron
PT   metabolism
XX
PS   Example 2; Fig 8; 209pp; English.
XX
CC   The present invention describes hereditary haemochromatosis gene
CC   products from the human haemochromatosis gene. The present sequence
CC   represents a hereditary haemochromatosis subregion from an individual
```

```
CC   unaffected by hereditary haemochromatosis (HH). Also described is a
CC   method to determine the presence or absence of the common hereditary
CC   haemochromatosis (HFE) gene mutation in an individual comprising:
CC   (a) providing DNA or RNA from the individual; and (b) assessing the
CC   DNA or RNA for the presence or absence of a haplotype or genotype where
CC   the presence or absence of the haplotype genotype indicates the likely
CC   presence of the HFE gene mutation in the genome of the individual. The
CC   HFE gene sequences from the present invention can be used to develop
CC   products for use in the diagnosis and treatment of HFE. The present
CC   invention also describes BTF genes, which are homologues of the milk
CC   protein butyrophilin (BT), and can be used in the production of agonists
CC   and antagonists of BT function. Also described are: (1) a RoRet gene
CC   which can be used to develop products for the study, diagnosis and
CC   treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC   which are homologues of a type 1 sodium transport gene, and can
CC   similarly be used for hypophosphatemia.
XX
SQ   Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;

  Query Match             100.0%;  Score 264;  DB 19;  Length 235033;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-76;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db      43388 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 43329

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43328 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 43269

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43268 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 43209

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43208 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43149

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db      43148 TGGAAAATCACAACCACAGCAAGG 43125


RESULT 13
AAV57903/c
ID   AAV57903 standard; DNA; 237326 BP.
XX
AC   AAV57903;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Hereditary haemochromatosis subregion from an HH affected individual.
XX
KW   Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW   diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW   BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW   type 1 sodium transport gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO9814466-A1.
XX
PD   09-APR-1998.
XX
PF   30-SEP-1997;   97WO-US17658.
XX
PR   07-MAY-1997;   97US-0852495.
PR   01-OCT-1996;   96US-0724394.
XX
PA   (PROG-) PROGENTIOR INC.
XX
PI   Feder JN,  Kronmal GS,  Lauer PM,  Ruddy DA,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1998-240014/21.
XX
PT   Hereditary haemochromatosis gene products - used to develop products
PT   for the diagnosis and treatment of hereditary disorders in iron
PT   metabolism
XX
PS   Claim 1; Fig 9; 209pp; English.
XX
CC   The present invention describes hereditary haemochromatosis gene
CC   products from the human haemochromatosis gene. The present sequence
CC   represents a hereditary haemochromatosis subregion from an hereditary
CC   haemochromatosis (HH) affected individual. Also described is a
CC   method to determine the presence or absence of the common hereditary
CC   haemochromatosis (HFE) gene mutation in an individual comprising:
CC   (a) providing DNA or RNA from the individual; and (b) assessing the
CC   DNA or RNA for the presence or absence of a haplotype or genotype where
CC   the presence or absence of the haplotype genotype indicates the likely
CC   presence of the HFE gene mutation in the genome of the individual. The
CC   HFE gene sequences from the present invention can be used to develop
CC   products for use in the diagnosis and treatment of HFE. The present
CC   invention also describes BTF genes, which are homologues of the milk
CC   protein butyrophilin (BT), and can be used in the production of agonists
CC   and antagonists of BT function. Also described are: (1) a RoRet gene
CC   which can be used to develop products for the study, diagnosis and
CC   treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC   which are homologues of a type 1 sodium transport gene, and can
CC   similarly be used for hypophosphatemia.
XX
SQ   Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;

  Query Match             100.0%;  Score 264;  DB 19;  Length 237326;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-76;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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RESULT 14
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ID   AAC68431 standard; DNA; 1440 BP.
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AC   AAC68431;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d2 mutation cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
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XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
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PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 347 A; 354 C; 408 G; 331 T; 0 other;

  Query Match             99.4%;  Score 262.4;  DB 22;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 3.2e-76;
  Matches  263;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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ID   AAC68432 standard; DNA; 1440 BP.
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AC   AAC68432;
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DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d1/2 mutation cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
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PF   04-APR-1997;   97US-0834497.
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PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 348 A; 354 C; 407 G; 331 T; 0 other;

  Query Match             99.4%;  Score 262.4;  DB 22;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 3.2e-76;
  Matches  263;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db        298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357

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Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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GenCore version 5.1.6

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Perfect score: 264
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Scoring table: IDENTITY_NUC
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Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	264	100.0	1440	13	US-10-138-888-10	Sequence 10, Appl
	3	264	100.0	2506	13	US-09-981-606-1	Sequence 1, Appli
	4	264	100.0	5982	14	US-10-016-634A-25	Sequence 25, Appl
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	20	100	37.9	100	13	US-10-273-228-110	Sequence 110, App
	21	98.4	37.3	100	13	US-10-272-665-111	Sequence 111, App
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ALIGNMENTS

RESULT 1
US-10-138-888-9
; Sequence 9, Application US/10138888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912

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;          FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Brian M. Poissant
;          REGISTRATION NUMBER: 28,462
;          REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 790-9090
;          TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 1440 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
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  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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RESULT 2
US-10-138-888-10
; Sequence 10, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Pennie & Edmonds LLP
;          STREET: 1155 Avenue of the Americas
;          CITY: New York
;          STATE: New York
;          COUNTRY: USA
;          ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/10/138,888
;          FILING DATE: 02-May-2002
;          CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US 08/834,497
;          FILING DATE: 04-APR-1997
;          APPLICATION NUMBER: US 08/652,265
;          FILING DATE: 23-MAY-1996
;          APPLICATION NUMBER: US 08/632,673
;          FILING DATE: 16-APR-1996
;          APPLICATION NUMBER: US 08/630,912
;          FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Brian M. Poissant
;          REGISTRATION NUMBER: 28,462
;          REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 790-9090
;          TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 1440 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;          NAME/KEY:  CDS
;          LOCATION:  222..1268
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;          NAME/KEY:  allele
;          LOCATION:  replace(1066, "a")
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;          /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-138-888-10

  Query Match             100.0%;  Score 264;  DB 13;  Length 1440;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-83;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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; GENERAL INFORMATION:
;  APPLICANT: Rothenberg et al.
;  TITLE OF INVENTION: Mutations associated with iron disorders
;  FILE REFERENCE: 24065-004CON
;  CURRENT APPLICATION NUMBER: US/09/981,606
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-981-606-1

  Query Match             100.0%;  Score 264;  DB 13;  Length 2506;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-83;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 136

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 196

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 256

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 316

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db        317 TGGAAAATCACAACCACAGCAAGG 340


RESULT 4
US-10-016-634A-25
; Sequence 25, Application US/10016634A
; Publication No. US20020192666A1
; GENERAL INFORMATION:
;  APPLICANT: Sun, Yongming
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Ghosh, Malavika
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Prc
;  FILE REFERENCE: DEX-0255
;  CURRENT APPLICATION NUMBER: US/10/016,634A
;  CURRENT FILING DATE:  2001-10-31
;  PRIOR APPLICATION NUMBER: US 60/244,258
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 176
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
;   LENGTH: 5982
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5780)..(5780)
;   OTHER INFORMATION: n=a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5885)..(5885)
;   OTHER INFORMATION: n=a, c, g or t
US-10-016-634A-25

  Query Match             100.0%;  Score 264;  DB 14;  Length 5982;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-83;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3402 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3461

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3462 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3521

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3522 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3581

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3582 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 3641

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       3642 TGGAAAATCACAACCACAGCAAGG 3665


RESULT 5
US-10-138-888-1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
```

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;         ATTORNEY/AGENT INFORMATION:
;              NAME: Brian M. Poissant
;              REGISTRATION NUMBER: 28,462
;              REFERENCE/DOCKET NUMBER: 8907-095-999
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212) 790-9090
;              TELEFAX: (212) 869-8864
;              OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;              (HH) protein"
;              /note= "No. US20030148972A1mal or wild-type (unaffected)
;              Hereditary Hemochromatosis (HH) gene
;              allele"
;         FEATURE:
;              NAME/KEY:  -
;              LOCATION:  140..7319
;         FEATURE:
;              NAME/KEY:  -
;              LOCATION:  5507..6023
;         FEATURE:
;              NAME/KEY:  allele
;              LOCATION:  replace(3878, "a")
;              OTHER INFORMATION:  /phenotype= "normal or wild-type
;              (unaffected)"
;              /label= 24d7
;         FEATURE:
;              NAME/KEY:  allele
;              LOCATION:  replace(5834, "g")
;              OTHER INFORMATION:  /phenotype= "normal or wild-type
;              (unaffected)"
;              /label= 24d1
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-138-888-1

  Query Match             100.0%;  Score 264;  DB 13;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-83;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAGG 4025


RESULT 6
US-10-138-888-3
;   GENERAL INFORMATION:
;         APPLICANT: Thomas, Winston J.
;                    Drayna, Dennis T.
;                    Feder, John N.
;                    Gnirke, Andreas
;                    Ruddy, David
;                    Tsuchihashi, Zenta
;                    Wolff, Roger K.
;         TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;         NUMBER OF SEQUENCES: 79
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Pennie & Edmonds LLP
;              STREET: 1155 Avenue of the Americas
;              CITY: New York
;              STATE: New York
;              COUNTRY: USA
;              ZIP: 10036-2711
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/138,888
;              FILING DATE: 02-May-2002
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/834,497
;              FILING DATE: 04-APR-1997
;              APPLICATION NUMBER: US 08/652,265
;              FILING DATE: 23-MAY-1996
;              APPLICATION NUMBER: US 08/632,673
;              FILING DATE: 16-APR-1996
;              APPLICATION NUMBER: US 08/630,912
;              FILING DATE: 04-APR-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Brian M. Poissant
;              REGISTRATION NUMBER: 28,462
;              REFERENCE/DOCKET NUMBER: 8907-095-999
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212) 790-9090
;              TELEFAX: (212) 869-8864
;              OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;              (HH) protein containing the 24d1
;              mutation"
;              /note= "Hereditary Hemochromatosis (HH)
;              gene 24d1 allele"
;         FEATURE:
;              NAME/KEY:  -
;              LOCATION:  140..7319
;         FEATURE:
;              NAME/KEY:  -
;              LOCATION:  5507..6023
;         SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-138-888-3

  Query Match             100.0%;  Score 264;  DB 13;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-83;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAGG 4025


RESULT 7
US-09-981-606-27
; Sequence 27, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
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;  APPLICANT: Rothenberg et al.
;  TITLE OF INVENTION: Mutations associated with iron disorders
;  FILE REFERENCE: 24065-004CON
;  CURRENT APPLICATION NUMBER: US/09/981,606
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 12146
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-981-606-27

  Query Match             100.0%;  Score 264;  DB 13;  Length 12146;
  Best Local Similarity   100.0%;  Pred. No. 3e-83;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4652 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 4711

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4712 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 4771

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4772 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 4831

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4832 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4891

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       4892 TGGAAAATCACAACCACAGCAAGG 4915


RESULT 8
US-10-301-844-1/c
; Sequence 1, Application US/10301844
; Publication No. US20030100747A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruddy, David A.
;                   Wolff, Roger K.
;        TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
;                            HEMOCHROMATOSIS GENE
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds, LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/301,844
;             FILING DATE: 20-No. US20030100747A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/852,495C
;             FILING DATE: 07-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-0057-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 235033 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-301-844-1

  Query Match             100.0%;  Score 264;  DB 15;  Length 235033;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-82;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43388 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 43329

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43328 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 43269

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43268 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 43209

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43208 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43149

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db      43148 TGGAAAATCACAACCACAGCAAGG 43125


RESULT 9
US-10-301-844-2/c
; Sequence 2, Application US/10301844
; Publication No. US20030100747A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruddy, David A.
;                   Wolff, Roger K.
;        TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
;                            HEMOCHROMATOSIS GENE
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds, LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/301,844
;             FILING DATE: 20-No. US20030100747A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/852,495C
;             FILING DATE: 07-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-0057-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
```

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;            TELEFAX: 650-493-5556
;            TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 237326 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-301-844-2

  Query Match             100.0%;  Score 264;  DB 15;  Length 237326;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-82;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43338 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 43279

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db      43278 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 43219

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43218 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 43159

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      43158 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43099

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db      43098 TGGAAAATCACAACCACAGCAAGG 43075


RESULT 10
US-10-138-888-11
; Sequence 11, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1440 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  222..1268
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(408, "g")
;             OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;             (HH)"
;             /label= 24d2
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-138-888-11

  Query Match             99.4%;  Score 262.4;  DB 13;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 4.5e-83;
  Matches  263;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        478 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db        538 TGGAAAATCACAACCACAGCAAGG 561


RESULT 11
US-10-138-888-12
; Sequence 12, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
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;           ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/138,888
;           FILING DATE: 02-May-2002
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/834,497
;           FILING DATE: 04-APR-1997
;           APPLICATION NUMBER: US 08/652,265
;           FILING DATE: 23-MAY-1996
;           APPLICATION NUMBER: US 08/632,673
;           FILING DATE: 16-APR-1996
;           APPLICATION NUMBER: US 08/630,912
;           FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Brian M. Poissant
;           REGISTRATION NUMBER: 28,462
;           REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 790-9090
;           TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1440 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;           NAME/KEY:  CDS
;           LOCATION:  222..1268
;       FEATURE:
;           NAME/KEY:  allele
;           LOCATION:  replace(408, "g")
;           OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;           (HH)"
;           /label= 24d2
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;           LOCATION:  replace(1066, "a")
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;           (HH)"
;           /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-138-888-12

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Db        298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        358 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGATGAGAGTC 417

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db        538 TGGAAAATCACAACCACAGCAAGG 561


RESULT 12
US-10-138-888-77
; Sequence 77, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Pennie & Edmonds LLP
;           STREET: 1155 Avenue of the Americas
;           CITY: New York
;           STATE: New York
;           COUNTRY: USA
;           ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/138,888
;           FILING DATE: 02-May-2002
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/834,497
;           FILING DATE: 04-APR-1997
;           APPLICATION NUMBER: US 08/652,265
;           FILING DATE: 23-MAY-1996
;           APPLICATION NUMBER: US 08/632,673
;           FILING DATE: 16-APR-1996
;           APPLICATION NUMBER: US 08/630,912
;           FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Brian M. Poissant
;           REGISTRATION NUMBER: 28,462
;           REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 790-9090
;           TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 77:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1440 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;           NAME/KEY:  CDS
;           LOCATION:  222..1268
;       FEATURE:
;           NAME/KEY:  allele
;           LOCATION:  replace(414, "t")
;           OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;           (HH)"
;           /label= 24d7
;       SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-138-888-77

  Query Match             99.4%;  Score 262.4;  DB 13;  Length 1440;
  Best Local Similarity   99.6%;  Pred. No. 4.5e-83;
  Matches  263;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db        478 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db        538 TGGAAAATCACAACCACAGCAAGG 561


RESULT 13
US-10-138-888-5
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;             OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;             (HH) protein containing the 24d2
;             mutation"
;             /note= "Hereditary Hemochromatosis (HH)
;             gene 24d2 allele"
;        FEATURE:
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;             LOCATION:  5507..6023
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-138-888-5

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  Best Local Similarity   99.6%;  Pred. No. 1.1e-82;
  Matches  263;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db       4002 TGGAAAATCACAACCACAGCAAGG 4025


RESULT 14
US-10-138-888-7
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
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;             TELEFAX: (212) 869-8864
;             OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;             (HH) protein containing both the 24d1
;             and 24d2 mutations"
;             /note= "Hereditary Hemochromatosis (HH)
;             gene containing a combination of both
;             24d1 and 24d2 alleles"
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;             NAME/KEY:  -
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;             (HH)"
;             /label= 24d1
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US-10-138-888-7

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  Best Local Similarity   99.6%;  Pred. No. 1.1e-82;
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Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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RESULT 15
US-10-138-888-79
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;             OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;             (HH) protein containing the 24d7 mutation"
;             /note= "Hereditary Hemochromatosis
;             (HH)gene 24d7 allele"
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  140..7319
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US-10-138-888-79

  Query Match             99.4%;  Score 262.4;  DB 13;  Length 10825;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-82;
  Matches  263;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	264	100.0	1440	3	US-08-652-265-10	Sequence 10, Appl
3	264	100.0	1440	3	US-08-834-497A-9	Sequence 9, Appli
4	264	100.0	1440	3	US-08-834-497A-10	Sequence 10, Appl
5	264	100.0	1440	3	US-09-503-444A-9	Sequence 9, Appli
6	264	100.0	1440	3	US-09-503-444A-10	Sequence 10, Appl
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9	264	100.0	10825	3	US-08-652-265-1	Sequence 1, Appli
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15	264	100.0	12146	4	US-09-277-457-27	Sequence 27, Appl
16	264	100.0	12146	4	US-09-679-729-27	Sequence 27, Appl
17	264	100.0	246240	2	US-08-724-394A-20	Sequence 20, Appl
18	264	100.0	246240	2	US-08-724-394A-21	Sequence 21, Appl
19	264	100.0	246240	2	US-08-724-394A-22	Sequence 22, Appl
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21	262.4	99.4	1440	3	US-08-652-265-12	Sequence 12, Appl
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23	262.4	99.4	1440	3	US-08-834-497A-12	Sequence 12, Appl
24	262.4	99.4	1440	3	US-09-503-444A-11	Sequence 11, Appl
25	262.4	99.4	1440	3	US-09-503-444A-12	Sequence 12, Appl
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38	40.6	15.4	264	3	US-09-244-093-1	Sequence 1, Appli
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41	40	15.2	40	3	US-08-834-497A-41	Sequence 41, Appl
42	40	15.2	40	3	US-09-503-444A-41	Sequence 41, Appl
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ALIGNMENTS

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RESULT 1
US-08-652-265-9
; Sequence 9, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "c")
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;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d2
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(414, "a")
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;       LOCATION:  replace(1066, "g")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
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;       OTHER INFORMATION:  /label= 24d1
US-08-652-265-9

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  Best Local Similarity   100.0%;  Pred. No. 2.5e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        538 TGGAAAATCACAACCACAGCAAGG 561


RESULT 2
US-08-652-265-10
; Sequence 10, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-10

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  Best Local Similarity   100.0%;  Pred. No. 2.5e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        538 TGGAAAATCACAACCACAGCAAGG 561


RESULT 3
US-08-834-497A-9
; Sequence 9, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  Windows 95
;       SOFTWARE:  FastSEQ for Windows Version 2.0b
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/834,497A
;       FILING DATE:  04-APR-1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/652,265
;       FILING DATE:  23-MAY-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/632,673
;       FILING DATE:  16-APR-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/630,912
;       FILING DATE:  04-APR-1996
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M.
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  8907-0056-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-493-4935
;       TELEFAX:  650-493-5556
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1440 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  222..1268
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;       NAME/KEY:  allele
;       LOCATION:  replace(408, "c")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d2
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(414, "a")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d7
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(1066, "g")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
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US-08-834-497A-9

  Query Match             100.0%;  Score 264;  DB 3;  Length 1440;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-79;
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Db        538 TGGAAAATCACAACCACAGCAAGG 561


RESULT 4
US-08-834-497A-10
; Sequence 10, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
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;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-10

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  Best Local Similarity  100.0%;  Pred. No. 2.5e-79;
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Db        538 TGGAAAATCACAACCACAGCAAGG 561


RESULT 5
US-09-503-444A-9
; Sequence 9, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
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;      NAME/KEY:  allele
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;      LOCATION:  replace(1066, "g")
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;      OTHER INFORMATION:  /label= 24d1
US-09-503-444A-9

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  Best Local Similarity  100.0%;  Pred. No. 2.5e-79;
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Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db        538 TGGAAAATCACAACCACAGCAAGG 561


RESULT 6
US-09-503-444A-10
; Sequence 10, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
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;       STREET:  1155 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  USA
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  Windows 95
;       SOFTWARE:  WordPerfect Version 8
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/503,444A
;       FILING DATE:  14-Feb-2000
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/652,265
;       FILING DATE:  23-May-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/632,673
;       FILING DATE:  16-Apr-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/630,912
;       FILING DATE:  04-Apr-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M.
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  8907-0088-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-790-9090
;       TELEFAX:  212-869-9741
;       TELEX:  66141
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1440 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  222..1268
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(1066, "a")
;       OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d1
US-09-503-444A-10

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  Best Local Similarity   100.0%;  Pred. No. 2.5e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db        298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        358 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 417

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Db        418 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 477

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db        478 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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RESULT 7
US-09-277-457-1
; Sequence 1, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 10653/002001
;  CURRENT APPLICATION NUMBER: US/09/277,457
;  CURRENT FILING DATE:  1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2506
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Missense mutation at nucleotide 314
US-09-277-457-1

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  Best Local Similarity   100.0%;  Pred. No. 3.2e-79;
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Db         77 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 136

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        137 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 196

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Db        197 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 256

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 316

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db        317 TGGAAAATCACAACCACAGCAAGG 340


RESULT 8
US-09-679-729-1
; Sequence 1, Application US/09679729
; Patent No. 6509442
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 24065-004 DIV
;  CURRENT APPLICATION NUMBER: US/09/679,729
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2506
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (0)...(0)
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;   OTHER INFORMATION: Missense mutation at nucleotide 314
US-09-679-729-1

  Query Match             100.0%;  Score 264;  DB 4;  Length 2506;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db         77 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 136

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        137 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 196

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 256

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db        257 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 316

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db        317 TGGAAAATCACAACCACAGCAAGG 340


RESULT 9
US-08-652-265-1
; Sequence 1, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= "No. 6025130mal or wild-type (unaffected)
;      OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;      OTHER INFORMATION:  allele"
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;      LOCATION:  140..7319
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;      OTHER INFORMATION:  normal or wild-type (unaffected) allele
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;      NAME/KEY:  -
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;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;      OTHER INFORMATION:  allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
;      OTHER INFORMATION:  allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3878, "a")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d7
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "g")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-1

  Query Match             100.0%;  Score 264;  DB 3;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db       4002 TGGAAAATCACAACCACAGCAAGG 4025
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RESULT 10
US-08-652-265-3
; Sequence 3, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d1 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d1 allele cDNA (SEQ ID NO:10)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(C) allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
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;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-3

  Query Match             100.0%;  Score 264;  DB 3;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db       4002 TGGAAAATCACAACCACAGCAAGG 4025


RESULT 11
US-08-834-497A-1
; Sequence 1, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
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;       NAME:  Poissant, Brian M.
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  8907-0056-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-493-4935
;       TELEFAX:  650-493-5556
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10825 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;       LOCATION:  6040..6153, 7107..7147)
;       OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /note= "No. 6140305mal or wild-type (unaffected)
;       OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;       OTHER INFORMATION:  allele"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  140..7319
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  normal or wild-type (unaffected) allele
;       OTHER INFORMATION:  cDNA (SEQ ID NO:9)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  3852..3891
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;       OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;       OTHER INFORMATION:  allele (SEQ ID NO:41)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  5507..6023
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;       OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
;       OTHER INFORMATION:  allele (SEQ ID NO:20)"
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(3872, "c")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d2
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(3878, "a")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d7
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(5834, "g")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d1
US-08-834-497A-1

  Query Match             100.0%;  Score 264;  DB 3;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db       4002 TGGAAAATCACAACCACAGCAAGG 4025


RESULT 12
US-08-834-497A-3
; Sequence 3, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
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;       NAME/KEY:  CDS
;       LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;       LOCATION:  6040..6153, 7107..7147)
;       OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  mutation"
;       OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;       OTHER INFORMATION:  gene 24d1 allele"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  140..7319
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  24d1 allele cDNA (SEQ ID NO:10)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  3852..3891
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d2(C) allele (SEQ ID NO:41)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  5507..6023
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(5834, "a")
;       OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d1
US-08-834-497A-3

  Query Match             100.0%;  Score 264;  DB 3;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAGG 4025


RESULT 13
US-09-503-444A-1
; Sequence 1, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= "No. 6228594mal or wild-type (unaffected)
;      OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;      OTHER INFORMATION:  allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) allele
;      OTHER INFORMATION:  cDNA (SEQ ID NO:9)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;      OTHER INFORMATION:  allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
;      OTHER INFORMATION:  allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
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;       OTHER INFORMATION:  /label= 24d2
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(3878, "a")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d7
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(5834, "g")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d1
US-09-503-444A-1

  Query Match             100.0%;  Score 264;  DB 3;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
              ||||||||||||||||||||||||
Db       4002 TGGAAAATCACAACCACAGCAAGG 4025


RESULT 14
US-09-503-444A-3
; Sequence 3, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d1 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d1 allele cDNA (SEQ ID NO:10)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(C) allele (SEQ ID NO:41)"
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;      NAME/KEY:  -
;      LOCATION:  5507..6023
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;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-09-503-444A-3

  Query Match             100.0%;  Score 264;  DB 3;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821

Qy         61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881

Qy        121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941

Qy        181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db       3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001

Qy        241 TGGAAAATCACAACCACAGCAAGG 264
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Db       4002 TGGAAAATCACAACCACAGCAAGG 4025


RESULT 15
US-09-277-457-27
; Sequence 27, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 10653/002001
;  CURRENT APPLICATION NUMBER: US/09/277,457
;  CURRENT FILING DATE:  1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 12146
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-277-457-27

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  Best Local Similarity   100.0%;  Pred. No. 6.5e-79;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 60
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Db        4652 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 4711

Qy          61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Db        4712 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 4771

Qy         121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
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Db        4772 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 4831

Qy         181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Db        4832 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4891

Qy         241 TGGAAAATCACAACCACAGCAAGG 264
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Db        4892 TGGAAAATCACAACCACAGCAAGG 4915


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Job time : 34.2837 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 14:08:55 ; Search time 2119.64 Seconds
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Perfect score: 434
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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4	432.4	99.6	653	9	HSHLAH4	Y09803 H.sapiens H
5	432.4	99.6	10825	6	AR117789	AR117789 Sequence
6	432.4	99.6	10825	6	AR117791	AR117791 Sequence
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18	430.8	99.3	10825	6	AR117792	AR117792 Sequence
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24	416.4	95.9	517	6	AR117804	AR117804 Sequence
25	416.4	95.9	517	6	AR149474	AR149474 Sequence
26	416.4	95.9	517	6	I82157	I82157 Sequence 3
27	415.4	95.7	517	6	I82167	I82167 Sequence 13
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33	330	76.0	360	6	AR097991	AR097991 Sequence
34	300.4	69.2	358	9	AF109385	AF109385 Homo sapi
35	277	63.8	1317	6	AX407339	AX407339 Sequence
36	276	63.6	809	9	HSA250635	AJ250635 Homo sapi
37	276	63.6	823	9	AF079408	AF079408 Homo sapi
38	276	63.6	860	9	AY205604	AY205604 Homo sapi
39	276	63.6	1073	9	HSA249337	AJ249337 Homo sapi
40	276	63.6	1085	9	HSA249336	AJ249336 Homo sapi
41	276	63.6	1200	9	AF115265	AF115265 Homo sapi
42	276	63.6	1280	9	HSA249335	AJ249335 Homo sapi
43	276	63.6	1440	6	AR117793	AR117793 Sequence
44	276	63.6	1440	6	AR117795	AR117795 Sequence
45	276	63.6	1440	6	AR149463	AR149463 Sequence

ALIGNMENTS

RESULT 1
AR199263
LOCUS AR199263 12146 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 27 from patent US 6355425.
ACCESSION AR199263
VERSION AR199263.1 GI:20249337
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12146)
AUTHORS Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.
TITLE Mutations associated with iron disorders
JOURNAL Patent: US 6355425-A 27 12-MAR-2002;
FEATURES Location/Qualifiers

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     source          1. .12146
                     /organism="unknown"
BASE COUNT     3383 a   2474 c   2911 g   3378 t
ORIGIN

  Query Match             100.0%;  Score 434;  DB 6;  Length 12146;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-130;
  Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       6494 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 6553

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       6554 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 6613

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 6673

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 6733

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       6734 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 6793

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       6794 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 6853

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       6854 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6913

Qy        421 TTTTTCTGTTTTAG 434
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Db       6914 TTTTTCTGTTTTAG 6927


RESULT 2
AR275782
LOCUS       AR275782               12146 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 27 from patent US 6509442.
ACCESSION   AR275782
VERSION     AR275782.1  GI:29709339
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12146)
  AUTHORS   Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.
  TITLE     Mutations associated with iron disorders
  JOURNAL   Patent: US 6509442-A 27 21-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .12146
                     /organism="unknown"
BASE COUNT     3383 a   2474 c   2911 g   3378 t
ORIGIN

  Query Match             100.0%;  Score 434;  DB 6;  Length 12146;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-130;
  Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       6494 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 6553

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       6554 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 6613

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 6673

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 6733

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       6734 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 6793

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       6794 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 6853

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6854 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6913

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6914 TTTTTCTGTTTTAG 6927


RESULT 3
HSHFE
LOCUS       HSHFE                  12146 bp    DNA     linear   PRI 23-JUL-1999
DEFINITION  Homo sapiens HFE gene.
ACCESSION   Z92910
VERSION     Z92910.1  GI:1890179
KEYWORDS    haemochromatosis; HFE gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 858)
  AUTHORS   Albig,W., Drabent,B., Burmester,N., Bode,C. and Doenecke,D.
  TITLE     The haemochromatosis candidate gene HFE (HLA-H) of man and mouse is
            located in syntenic regions within the histone gene cluster
  JOURNAL   J. Cell. Biochem. 69 (2), 117-126 (1998)
  MEDLINE   98208340
   PUBMED   9548560
REFERENCE   2  (bases 1 to 12146)
  AUTHORS   Albig,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-1997) Albig W., Georg-August-Universitaet
            Goettingen, Biochemie und Molekulare Zellbiologie, Humboldtallee
            23, Goettingen, FRG, 37073
FEATURES             Location/Qualifiers
     source          1. .12146
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p"
                     /clone="ICRFy901D1223"
                     /clone_lib="ICRF YAC-library"
     gene            1028. .10637
                     /gene="HFE"
     exon            1028. .1324
                     /gene="HFE"
                     /number=1
     CDS             join(1249. .1324,4652. .4915,5125. .5400,6494. .6769,
                     6928. .7041,7995. .8035)
                     /gene="HFE"
                     /function="iron metabolism"
                     /note="haemochromatosis candidate gene"
                     /codon_start=1
                     /protein_id="CAB07442.1"
                     /db_xref="GI:1890180"
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                     RAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTS
                     SVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGE
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                     SRGAMGHYVLAERE"
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                     /number=1
     repeat_unit     3494. .3735
                     /gene="HFE"
                     /rpt_family="Alu"
     repeat_unit     3973. .4283
                     /gene="HFE"
                     /rpt_family="Alu"
     exon            4652. .4915
                     /gene="HFE"
                     /number=2
     intron          4916. .5124
                     /gene="HFE"
                     /number=2
     exon            5125. .5400
                     /gene="HFE"
                     /number=3
     intron          5401. .6493
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     repeat_unit     5707. .6005
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                     /rpt_family="Alu"
     exon            6494. .6769
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     intron          6770. .6927
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     exon            6928. .7041
                     /gene="HFE"
                     /number=5
     intron          7042. .7994
                     /gene="HFE"
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     exon            7995. .9050
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     repeat_unit     9017. .9340
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     intron          9051. .10205
                     /gene="HFE"
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     repeat_unit     9957. .10239
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     exon            10206. .10637
                     /gene="HFE"
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     polyA_signal    10617. .10622
                     /gene="HFE"
BASE COUNT     3383 a    2474 c    2911 g    3378 t
ORIGIN

  Query Match             100.0%;  Score 434;  DB 9;  Length 12146;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-130;
  Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6494 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 6553

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       6554 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 6613

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 6673

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 6733

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6734 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 6793

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6794 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 6853

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       6854 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6913

Qy        421 TTTTTCTGTTTTAG 434
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Db       6914 TTTTTCTGTTTTAG 6927


RESULT 4
HSHLAH4
LOCUS       HSHLAH4                  653 bp    DNA     linear   PRI 23-JUL-1999
DEFINITION  H.sapiens HFE gene, exon 4 & 5.
ACCESSION   Y09803
VERSION     Y09803.1  GI:2370113
KEYWORDS    HFE gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Carella and Gasparini,P.
  TITLE     Hereditary hemochromatosis genomic structure and organization of
            HLA-H gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 653)
  AUTHORS   Gasparini,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-DEC-1996) P. Gasparini, Servizio de Genetica Medica -
            IRCCS, 'Ospedale CSS', Via Cappuccini, 71013 S Giovanni, Rotondo
            (FG), ITALY
COMMENT     Related sequence: U60319.
FEATURES             Location/Qualifiers
     source          1. .653
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="6p22"
                     /clone_lib="31H6"
     gene            51. .598
                     /gene="HFE"
     exon            51. .326
                     /gene="HFE"
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                     /usedin=Y09801:hfe_mrna
                     /label=ex4
     exon            485. .598
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ORIGIN

  Query Match             99.6%;  Score 432.4;  DB 9;  Length 653;
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  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db         51 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 110

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db        111 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 170

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db        171 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 230

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db        231 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 290

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db        291 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 350

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db        351 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 410

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db        411 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 470

Qy        421 TTTTTCTGTTTTAG 434
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Db        471 TTTTTCTGTTTTAG 484


RESULT 5
AR117789
LOCUS       AR117789               10825 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6140305.
ACCESSION   AR117789
VERSION     AR117789.1  GI:14098695
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 1 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .10825
                     /organism="unknown"
BASE COUNT     2998 a   2253 c   2648 g   2926 t
ORIGIN

  Query Match             99.6%;  Score 432.4;  DB 6;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-129;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 6
AR117791
LOCUS       AR117791               10825 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 5 from patent US 6140305.
ACCESSION   AR117791
VERSION     AR117791.1  GI:14098697
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 5 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .10825
                     /organism="unknown"
BASE COUNT     2998 a   2252 c   2649 g   2926 t
ORIGIN

  Query Match             99.6%;  Score 432.4;  DB 6;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-129;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025
```

```
Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039


RESULT 7
AR149459
LOCUS       AR149459               10825 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6228594.
ACCESSION   AR149459
VERSION     AR149459.1  GI:15114050
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 1 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .10825
                     /organism="unknown"
BASE COUNT     2998 a   2253 c   2648 g   2926 t
ORIGIN

  Query Match             99.6%;  Score 432.4;  DB 6;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-129;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039


RESULT 8
AR149461
LOCUS       AR149461               10825 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 5 from patent US 6228594.
ACCESSION   AR149461
VERSION     AR149461.1  GI:15114052
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 5 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .10825
                     /organism="unknown"
BASE COUNT     2998 a   2252 c   2649 g   2926 t
ORIGIN

  Query Match             99.6%;  Score 432.4;  DB 6;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-129;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039


RESULT 9
AL359892/c
LOCUS       AL359892               193752 bp    DNA     linear   HTG 13-JUN-2001
DEFINITION  Homo sapiens chromosome 6 clone RP11-557F22, *** SEQUENCING IN
            PROGRESS ***, 18 unordered pieces.
ACCESSION   AL359892
VERSION     AL359892.5  GI:9930971
KEYWORDS    HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sims,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Aug 27, 2000 this sequence version replaced gi:9864230.
            -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
```

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            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bA557F22
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 183925 bases at least Q40
            Consensus quality: 187703 bases at least Q30
            Consensus quality: 189658 bases at least Q20
            Insert size: 192052; sum-of-contigs
            Insert size: 198247; agarose-fp
            Quality coverage: 3.68x in Q20 bases; sum-of-contigs Quality
            coverage: 3.70x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 18 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     3250: contig of 3250 bp in length
            *     3251     3350: gap of 100 bp
            *     3351    14600: contig of 11250 bp in length
            *    14601    14700: gap of 100 bp
            *    14701    32357: contig of 17657 bp in length
            *    32358    32457: gap of 100 bp
            *    32458    34886: contig of 2429 bp in length
            *    34887    34986: gap of 100 bp
            *    34987    43490: contig of 8504 bp in length
            *    43491    43590: gap of 100 bp
            *    43591    47437: contig of 3847 bp in length
            *    47438    47537: gap of 100 bp
            *    47538    57356: contig of 9819 bp in length
            *    57357    57456: gap of 100 bp
            *    57457    59845: contig of 2389 bp in length
            *    59846    59945: gap of 100 bp
            *    59946    63972: contig of 4027 bp in length
            *    63973    64072: gap of 100 bp
            *    64073    82711: contig of 18639 bp in length
            *    82712    82811: gap of 100 bp
            *    82812   111814: contig of 29003 bp in length
            *   111815   111914: gap of 100 bp
            *   111915   120276: contig of 8362 bp in length
            *   120277   120376: gap of 100 bp
            *   120377   136660: contig of 16284 bp in length
            *   136661   136760: gap of 100 bp
            *   136761   153913: contig of 17153 bp in length
            *   153914   154013: gap of 100 bp
            *   154014   158659: contig of 4646 bp in length
            *   158660   158759: gap of 100 bp
            *   158760   164235: contig of 5476 bp in length
            *   164236   164335: gap of 100 bp
            *   164336   184996: contig of 20661 bp in length
            *   184997   185096: gap of 100 bp
            *   185097   193752: contig of 8656 bp in length.
FEATURES             Location/Qualifiers
     source          1. .193752
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /clone="RP11-557F22"
                     /clone_lib="RPCI-11.2"
     misc_feature    1. .3250
                     /note="assembly_fragment:01752
                     fragment_chain:1"
     misc_feature    3351. .14600
                     /note="assembly_fragment:01177
                     fragment_chain:1"
     misc_feature    14701. .32357
                     /note="assembly_fragment:00673
                     fragment_chain:1"
     misc_feature    32458. .34886
                     /note="assembly_fragment:00884
                     fragment_chain:1"
     misc_feature    34987. .43490
                     /note="assembly_fragment:00652
                     fragment_chain:1"
     misc_feature    43591. .47437
                     /note="assembly_fragment:00628
                     fragment_chain:1"
     misc_feature    47538. .57356
                     /note="assembly_fragment:00983
                     fragment_chain:2"
     misc_feature    57457. .59845
                     /note="assembly_fragment:01129
                     fragment_chain:2"
     misc_feature    59946. .63972
                     /note="assembly_fragment:01207
                     fragment_chain:3"
     misc_feature    64073. .82711
                     /note="assembly_fragment:00301
                     fragment_chain:3"
     misc_feature    82812. .111814
                     /note="assembly_fragment:00470"
     misc_feature    111915. .120276
                     /note="assembly_fragment:00783.0"
     misc_feature    120377. .136660
                     /note="assembly_fragment:01014"
     misc_feature    136761. .153913
                     /note="assembly_fragment:01161"
     misc_feature    154014. .158659
                     /note="assembly_fragment:01329"
     misc_feature    158760. .164235
                     /note="assembly_fragment:01675"
     misc_feature    164336. .184996
                     /note="assembly_fragment:01884"
     misc_feature    185097. .193752
                     /note="assembly_fragment:01893"
BASE COUNT    55929 a  40409 c  39996 g  55686 t   1732 others
ORIGIN

  Query Match             99.6%;  Score 432.4;  DB 2;  Length 193752;
  Best Local Similarity   99.8%;  Pred. No. 3.3e-129;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11047 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 10988

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10987 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 10928

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10927 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 10868

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10867 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 10808

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10807 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 10748

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10747 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 10688

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
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Db      10687 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 10628

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db      10627 TTTTTCTGTTTTAG 10614


RESULT 10
BD084121/c
LOCUS       BD084121              235033 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084121
VERSION     BD084121.1  GI:22629731
KEYWORDS    JP 2001525663-A/9.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 235033)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 9 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/9
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US    08/724394,07-MAY-1997 US    08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
            FH   Key             Location/Qualifiers
            FT   source          1. .235033
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .235033
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT    68800 a  48442 c  47837 g  69954 t
ORIGIN

  Query Match             99.6%;  Score 432.4;  DB 6;  Length 235033;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-129;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41544 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 41485

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41484 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 41425

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41424 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 41365

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41364 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 41305

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41304 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 41245

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41244 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 41185

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      41184 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 41125

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db      41124 TTTTTCTGTTTTAG 41111


RESULT 11
AR036572
LOCUS       AR036572              246240 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 20 from patent US 5872237.
ACCESSION   AR036572
VERSION     AR036572.1  GI:5953240
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 246240)
  AUTHORS   Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
            Thomas,W., Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Megabase transcript map: novel sequences and antibodies thereto
  JOURNAL   Patent: US 5872237-A 20 16-FEB-1999;
FEATURES              Location/Qualifiers
     source           1. .246240
                      /organism="unknown"
BASE COUNT    73211 a  50177 c  50599 g  72252 t      1 others
ORIGIN

  Query Match             99.6%;  Score 432.4;  DB 6;  Length 246240;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-129;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197909 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 197968

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197969 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 198028

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198029 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 198088

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198089 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 198148

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198149 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 198208

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198209 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 198268

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     198269 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 198328

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db     198329 TTTTTCTGTTTTAG 198342


RESULT 12
AR036573
LOCUS       AR036573              246240 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 21 from patent US 5872237.
ACCESSION   AR036573
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VERSION     AR036573.1  GI:5953241
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 246240)
  AUTHORS   Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
            Thomas,W., Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Megabase transcript map: novel sequences and antibodies thereto
  JOURNAL   Patent: US 5872237-A 21 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .246240
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BASE COUNT    73211 a  50177 c  50599 g  72252 t      1 others
ORIGIN

  Query Match            99.6%;  Score 432.4;  DB 6;  Length 246240;
  Best Local Similarity  99.8%;  Pred. No. 3.4e-129;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db     197909 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 197968

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db     197969 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 198028

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Qy        421 TTTTTCTGTTTTAG 434
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RESULT 13
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DEFINITION  Sequence 22 from patent US 5872237.
ACCESSION   AR036574
VERSION     AR036574.1  GI:5953242
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 246240)
  AUTHORS   Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
            Thomas,W., Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Megabase transcript map: novel sequences and antibodies thereto
  JOURNAL   Patent: US 5872237-A 22 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .246240
                     /organism="unknown"
BASE COUNT    73211 a  50177 c  50599 g  72252 t      1 others
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  Best Local Similarity  99.8%;  Pred. No. 3.4e-129;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db     198209 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 198268

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db     198329 TTTTTCTGTTTTAG 198342


RESULT 14
HSU91328/c
LOCUS       HSU91328              246282 bp    DNA     linear   PRI 17-DEC-2001
DEFINITION  Human hereditary haemochromatosis region, histone 2A-like protein
            gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and
            sodium phosphate transporter (NPT3) gene, complete cds.
ACCESSION   U91328
VERSION     U91328.1  GI:2088550
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 246282)
  AUTHORS   Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quintana,L.,
            Domingo,R. Jr., Meyer,N.C., Irrinki,A., McClelland,E.E., Fullan,A.,
            Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C.,
            Tsuchihashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J.N.
  TITLE     A 1.1-Mb transcript map of the hereditary hemochromatosis locus
  JOURNAL   Genome Res. 7 (5), 441-456 (1997)
  MEDLINE   97294057
   PUBMED   9149941
REFERENCE   2  (bases 1 to 246282)
  AUTHORS   Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quintana,L.,
            Domingo,R. Jr., Meyer,N.C., Irrinke,A., McClelland,E.E., Fullan,A.,
            Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C.,
            Tsuchihashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-FEB-1997) Sequencing, Mercator Genetics, 4040
            Campbell Avenue, Menlo Park, CA 94025, USA
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Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Qy        421 TTTTTCTGTTTTAG 434
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RESULT 15
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DEFINITION  Homo sapiens hereditary hemochromatosis protein precursor (HFE)
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ACCESSION   AF525499
VERSION     AF525499.1  GI:22094648
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  ORGANISM  Homo sapiens
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  AUTHORS   Kutlar,F., Glendenning,M. and Kutlar,A.
  TITLE     Heterozygote T->C mutation was detected at the intron 4 of the
            human hemachromatosis gene in an Africa American individual
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 733)
  AUTHORS   Kutlar,F., Glendenning,M. and Kutlar,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2002) Medicine/Hematology-Oncology/Hemoglobin DNA
            Laboratory, Medical College of Georgia, 15th street, AC-1000,
            Augusta, GA 30912, USA
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23: em_gss_mus:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	276	63.6	729	14	CB529554	CB529554 UI-H-FT2-
	2	251.4	57.9	819	10	BG747345	BG747345 602704818
	3	243	56.0	570	10	BE272926	BE272926 601171213
	4	226	52.1	668	12	BM723847	BM723847 UI-E-EO1-
c	5	167.6	38.6	444	28	AZ025590	AZ025590 RPCI-23-3
	6	165.6	38.2	1719	11	AK088986	AK088986 Mus muscu
	7	165.6	38.2	1723	11	AK009581	AK009581 Mus muscu
c	8	154	35.5	536	28	AZ074871	AZ074871 RPCI-23-4
c	9	148.8	34.3	481	28	AZ025784	AZ025784 RPCI-23-3
	10	105.2	24.2	831	12	BI452668	BI452668 603169877
c	11	88	20.3	611	14	CB469137	CB469137 sn03_F06.
	12	88	20.3	877	14	CD245388	CD245388 AGENCOURT
	13	86.6	20.0	490	10	BE487497	BE487497 176270 BA
	14	86.2	19.9	752	29	AB005947	AB005947 Mouse gen
	15	85.2	19.6	467	12	BM694948	BM694948 UI-E-CI1-
c	16	85.2	19.6	653	9	AW514210	AW514210 hd75b05.x
	17	85	19.6	591	10	BF854420	BF854420 MR2-EN009
	18	84.6	19.5	390	10	BF808068	BF808068 IL5-CI015
c	19	84.6	19.5	456	10	BF753297	BF753297 QV3-CT055
c	20	84.6	19.5	510	9	AW516790	AW516790 xq04c07.x
	21	84.6	19.5	530	9	AL035930	AL035930 DKFZp564A
c	22	84.6	19.5	551	9	AI978686	AI978686 wr58c07.x
	23	84.6	19.5	574	10	BG425317	BG425317 602447230
c	24	84.6	19.5	597	14	CD365590	CD365590 UI-H-FT2-
c	25	84.6	19.5	628	9	AI954031	AI954031 wx78g05.x
	26	84.6	19.5	667	10	BG742120	BG742120 602633590
	27	84.6	19.5	684	10	BG744060	BG744060 602722842
c	28	84.6	19.5	687	12	BM985243	BM985243 UI-CF-EC1
c	29	84.6	19.5	699	14	CB528356	CB528356 UI-H-FT2-
	30	84.6	19.5	757	10	BG681820	BG681820 602629749
	31	84.6	19.5	816	14	CD245399	CD245399 AGENCOURT
c	32	84.6	19.5	821	10	BG744821	BG744821 602722954
	33	84.6	19.5	826	12	BI185105	BI185105 UNL-P-FN-
	34	84.6	19.5	840	10	BG682598	BG682598 602626733
	35	84.6	19.5	906	14	CD517051	CD517051 AGENCOURT
c	36	84.6	19.5	911	9	AL561819	AL561819 AL561819
	37	84.6	19.5	912	9	AI557260	AI557260 PT2.1_15_
	38	84.6	19.5	912	13	BQ668524	BQ668524 AGENCOURT
	39	84.6	19.5	916	10	BG744157	BG744157 602722954
	40	84.6	19.5	1009	9	AL540488	AL540488 AL540488
c	41	84.6	19.5	1049	9	AL580556	AL580556 AL580556
c	42	84.6	19.5	1092	9	AL574938	AL574938 AL574938
	43	84.6	19.5	1158	10	BF038889	BF038889 601461404
	44	84.6	19.5	1172	10	BG165057	BG165057 602343445
c	45	84.6	19.5	1200	9	AL526608	AL526608 AL526608

ALIGNMENTS

RESULT 1
CB529554/c
LOCUS CB529554 729 bp mRNA linear EST 16-MAY-2003
DEFINITION UI-H-FT2-bjh-m-12-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone UI-H-FT2-bjh-m-12-0-UI 3', mRNA sequence.
ACCESSION CB529554
VERSION CB529554.1 GI:29390357
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 729)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.

```
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjh-m-12-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     subtracted according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. The tissue was provided by Dr.
                     Gary W. Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT2
                     TAG_TISSUB=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      151 a    211 c    165 g    202 t
ORIGIN

  Query Match             63.6%;  Score 276;  DB 14;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-67;
  Matches  276;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 511

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 451

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 391

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 331

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 276
              ||||||||||||||||||||||||||||||||||
Db        330 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 295


RESULT 2
BG747345
LOCUS       BG747345                819 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602704818F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857941 5',
            mRNA sequence.
ACCESSION   BG747345
VERSION     BG747345.1  GI:14057998
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1711  row: d  column: 06
            High quality sequence stop: 792.
FEATURES             Location/Qualifiers
     source          1. .819
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4857941"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_15"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT      202 a    201 c    235 g    181 t
ORIGIN

  Query Match             57.9%;  Score 251.4;  DB 10;  Length 819;
  Best Local Similarity   98.9%;  Pred. No. 5.2e-60;
  Matches  274;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 513

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        514 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAG-CAA 572

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        573 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCA-G 631

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 691

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGG 277
              |||||||||||||||||||||||||||||||||| |||
Db        692 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTTGGG 728


RESULT 3
BE272926
LOCUS       BE272926                570 bp    mRNA    linear   EST 13-JUL-2000
DEFINITION  601171213F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3544803 5',
            mRNA sequence.
ACCESSION   BE272926
VERSION     BE272926.1  GI:9147279
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 570)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM240  row: j  column: 04
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```
          High quality sequence stop: 566.
FEATURES             Location/Qualifiers
     source          1. .570
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3544803"
                     /tissue_type="renal cell adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_14"
                     /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      140 a    148 c    175 g    107 t
ORIGIN

  Query Match             56.0%;  Score 243;  DB 10;  Length 570;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-57;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 386

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 446

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 506

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 566

Qy        241 ACC 243
              |||
Db        567 ACC 569


RESULT 4
BM723847
LOCUS       BM723847                668 bp    mRNA    linear   EST 01-MAR-2002
DEFINITION  UI-E-EO1-aix-h-17-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone
            UI-E-EO1-aix-h-17-0-UI 5', mRNA sequence.
ACCESSION   BM723847
VERSION     BM723847.1  GI:19045178
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 668)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .668
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EO1-aix-h-17-0-UI"
                     /tissue_type="fetal eye"
                     /dev_stage="fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-EO1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EO1 is a normalized cDNA library containing the
                     following tissue(s): fetal eye. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CGCGTATACC. This library was created for the program, Gene
                     Discovery in the Visual System, supported by National Eye
                     Institute (NEI)."
BASE COUNT      164 a    166 c    167 g    171 t
ORIGIN

  Query Match             52.1%;  Score 226;  DB 12;  Length 668;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-53;
  Matches  226;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 CTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGAT 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGAT 60

Qy        111 AAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGG 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGG 120

Qy        171 ACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGC 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGC 180

Qy        231 CAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 276
              |||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 226


RESULT 5
AZ025590/c
LOCUS       AZ025590                444 bp    DNA     linear   GSS 25-FEB-2000
DEFINITION  RPCI-23-316A10.TV RPCI-23 Mus musculus genomic clone RPCI-23-316A10
            , genomic survey sequence.
ACCESSION   AZ025590
VERSION     AZ025590.1  GI:7100974
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 444)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
```

```
  JOURNAL   Unpublished
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 316  row: A  column: 10
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .444
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-316A10"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).   "
BASE COUNT      110 a    126 c    110 g     97 t      1 others
ORIGIN

  Query Match             38.6%;  Score 167.6;  DB 28;  Length 444;
  Best Local Similarity   75.2%;  Pred. No. 1.8e-36;
  Matches  209;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||| |||||||||| |||||  |   ||    | ||||| | | |||| |||||  ||||||
Db        324 TGCCTACTTTGGTGAAAGTGACTCGCCACTGGGCCTCTACGGGGACCTCTCTCTAAGGTGTC 265

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              |||  || ||| || ||||||||||||||| |||| |||| ||||||| || || |||
Db        264 AGGCTCTGGACTTCTTCCCCCAGAACATCACTATGAGGTGGTTGAAGGACAACCAACCAC 205

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              |||||||||| ||  || | ||  |  | ||  | || || ||||||| |||||| || |
Db        204 TGGATGCCAAAGATGTCAACCCCGAGAAGGTGCTACCTAACGGGGATGAGACCTATCAAG 145

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||| ||||  |||| ||  |||||||||| |||   || |  || || || |||||||
Db        144 GCTGGCTAACAATGGCCGTGGCCCCTGGGGACGAGACAAGGTTCACCTGTCAAGTGGAGC 85

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGT 278
              |||||||||||| ||||| |||| ||     ||||||
Db         84 ACCCAGGCCTGGACCAGCCTCTCACTGCCTCTTGGGGT 47


RESULT 6
AK088986
LOCUS       AK088986               1719 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN
            full-length enriched library, clone:E430034J19
            product:hemochromatosis, full insert sequence.
ACCESSION   AK088986
VERSION     AK088986.1  GI:26354115
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1719)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
```

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  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
     source          1. .1719
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="NOD"
                     /db_xref="FANTOM_DB:E430034J19"
                     /db_xref="taxon:10090"
                     /clone="E430034J19"
                     /cell_type="thymic cells"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="2 days neonate"
     CDS             97. .1173
                     /note="unnamed protein product; hemochromatosis
                     (MGD|MGI:109191)
                     putative"
                     /codon_start=1
                     /protein_id="BAC40688.1"
                     /db_xref="GI:26354116"
                     /translation="MSLSAGLPVRPLLLLLLLWSVAPQALPPRSHSLRYLFMGASEPD
                     LGLPLFEARGYVDDQLFVSYNHESRRAEPRAPWILEQTSSQLWLHLSQSLKGWDYMFI
                     VDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWRYGYDGQDHLEFC
                     PKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLELGRGVLGQQVP
                     TLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVLPNGDETYQ
                     GWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVGI
                     LFLILRKRKASGGTMGGYVLTDCE"
     polyA_signal    1690. .1695
                     /note="putative"
     polyA_site      1719
                     /note="putative"
BASE COUNT      405 a    452 c    455 g    407 t
ORIGIN

  Query Match             38.2%;  Score 165.6;  DB 11;  Length 1719;
  Best Local Similarity   75.0%;  Pred. No. 1.1e-35;
  Matches  207;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||| |||||||||| ||||| |  ||   | ||||| | | |||| ||||| ||||||
Db        746 TGCCTACTTTGGTGAAAGTGACTCGCCACTGGGCCTCTACGGGGACCTCTCTAAGGTGTC 805

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
                |||  || ||| || ||||||||||||||| |||| |||| ||||||| || || |||
Db        806 AGGCTCTGGACTTCTTCCCCCAGAACATCACTATGAGGTGGTTGAAGGACAACCAACCAC 865

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              |||||||||| ||  || | ||  |  | ||  |||| || || |||| |||||| || |
Db        866 TGGATGCCAAAGATGTCAACCCCGAGAAGGTGCTGCCTAACGGAGATGAGACCTATCAAG 925

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||| | || ||||| ||  |||||||||| |||   || |  || || || |||||||
Db        926 GCTGGCTGACGTTGGCAGTGGCCCCTGGGGACGAGACAAGGTTCACCTGTCAAGTGGAGC 985

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 276
              |||||||||||| ||||| |||| ||     ||||
Db        986 ACCCAGGCCTGGACCAGCCTCTCACTGCCTCTTGGG 1021


RESULT 7
AK009581
LOCUS       AK009581               1723 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
            library, clone:2310032M04 product:hemochromatosis, full insert
            sequence.
ACCESSION   AK009581
VERSION     AK009581.1  GI:12844462
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
```

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  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1723)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:2310032M04"
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                     /clone="2310032M04"
                     /sex="male"
                     /tissue_type="tongue"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
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                     (MGD|MGI:109191)
                     putative"
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                     /db_xref="MGI:109191"
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                     DLGLPLFEARGYVDDQLFVSYNHESRRAEPRAPWILEQTSSQLWLHLSQSLKGWDYMF
                     IVDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWRYGYDGQDHLEF
                     CPKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLELGRGVLGQQV
                     PTLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVLPNGDETY
                     QGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVG
                     ILFLILRKRKASGGTMGGYVLTDCE"
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                     /note="putative"
     polyA_site      1723
                     /note="putative"
BASE COUNT      406 a    456 c    454 g    407 t
ORIGIN

  Query Match             38.2%;  Score 165.6;  DB 11;  Length 1723;
  Best Local Similarity   75.0%;  Pred. No. 1.1e-35;
  Matches  207;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||| |||||||||| ||||| |  ||   | |||| | | |||| |||| ||||||
Db        751 TGCCTACTTTGGTGAAAGTGACTCGCCACTGGGCCTCTACGGGGACCTCTCTAAGGTGTC 810

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
               |||  || ||| || ||||||||||||||| |||| |||| ||||||| || || |||
Db        811 AGGCTCTGGACTTCTTCCCCCAGAACATCACTATGAGGTGGTTGAAGGACAACCAACCAC 870

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              |||||||||| ||  || | ||  |  | ||  | || || |||||| |||||| || |
Db        871 TGGATGCCAAAGATGTCAACCCCGAGAAGGTGCTACCTAACGGGGATGAGACCTATCAAG 930

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||| | || ||||| ||  |||||||||| |||   || |  || || || |||||||
Db        931 GCTGGCTGACATTGGCCGTGGCCCCTGGGGACGAGACAAGGTTCACCTGTCAAGTGGAGC 990

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 276
              |||||||||||| ||||| |||| ||     ||||
Db        991 ACCCAGGCCTGGACCAGCCTCTCACTGCCTCTTGGG 1026


RESULT 8
AZ074871/c
LOCUS       AZ074871                 536 bp    DNA     linear   GSS 31-MAR-2000
DEFINITION  RPCI-23-408J22.TJ RPCI-23 Mus musculus genomic clone RPCI-23-408J22
            , genomic survey sequence.
ACCESSION   AZ074871
VERSION     AZ074871.1  GI:7367768
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 536)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished
COMMENT     Other_GSSs: RPCI-23-408J22.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 408  row: J  column: 22
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
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                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
```

EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
BASE COUNT 148 a 149 c 124 g 114 t 1 others
ORIGIN

Query Match 35.5%; Score 154; DB 28; Length 536;
Best Local Similarity 74.5%; Pred. No. 1.4e-32;
Matches 207; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

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Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||| |||||||||| ||||| |  ||   | ||||| | | |||| ||||| ||||||
Db        341 TGCCTACTTTGGTGAAAGTGACTCGCCACTGGGCCTCTACGGGGACCTCTCTAAGGTGTC 282

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
               |||  || ||| || ||||||||||||||| |||| |||| ||||||| || || |||
Db        281 AGGCTCTGGACTTCTTCCCCCAGAACATCACTATGAGGTGGTTGAAGGACAACCAACCAC 222

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              |||||||||| ||  || | ||  |  | ||  | || || ||||||| |||||| || |
Db        221 TGGATGCCAAAGATGTCAACCCCGAGAAGGTGCTACCTAACGGGGATGAGACCTATCAAG 162

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              |||||||  | ||  | ||  |||||||||| |||   || |  || || || |||||||
Db        161 GCTGGAT-GCATTAACCGTGGCCCCTGGGGACGAGACAAGGTTCACCTGTCAAGTGGAGC 103

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGT 278
              |||||||||||| ||||| |||| ||      ||||||
Db        102 ACCCAGGCCTGGACCAGCCTCTCACTGCCTCTTGGGGT 65
```

RESULT 9
AZ025784/c
LOCUS AZ025784 481 bp DNA linear GSS 25-FEB-2000
DEFINITION RPCI-23-316C10.TV RPCI-23 Mus musculus genomic clone RPCI-23-316C10 , genomic survey sequence.
ACCESSION AZ025784
VERSION AZ025784.1 GI:7101168
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 481)
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished
COMMENT Other_GSSs: RPCI-23-316C10.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 316 row: C column: 10
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .481
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-316C10"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
BASE COUNT 126 a 135 c 112 g 108 t
ORIGIN

Query Match 34.3%; Score 148.8; DB 28; Length 481;
Best Local Similarity 73.4%; Pred. No. 3.9e-31;
Matches 204; Conservative 0; Mismatches 72; Indels 2; Gaps 1;

```
Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||| |||||||||| ||||| |  ||   | ||||| | | |||| ||||| ||||||
Db        340 TGCCTACTTTGGTGAAAGTGACTCGCCACTGGGCCTCTACGGGGACCTCTCTAAGGTGTC 281

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
               |||  || ||| || ||||||||||||||| |||| |||| ||||||| || || |||
Db        280 AGGCTCTGGACTTCTTCCCCCAGAACATCACTATGAGGTGGTTGAAGGACAACCAACCAC 221

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              |||||||||| ||  || | ||  |  | ||  | || || ||||||| |||||| || |
Db        220 TGGATGCCAAAGATGTCAACCCCGAGAAGGTGCTACCTAACGGGAATGAGACCTATCAAG 161

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              |||||  |||    |   ||  |||||||||| |||   || |  || || || |||||||
Db        160 GCTGGCTAA--AAGAAAGTGGCCCCTGGGGACGAGACAAGGTTCACCTGTCAAGTGGAGC 103

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGT 278
              |||||||||||| ||||| |||| ||      ||||||
Db        102 ACCCAGGCCTGGACCAGCCTCTCACTGCCTCTTGGGGT 65
```

RESULT 10
BI452668
LOCUS BI452668 831 bp mRNA linear EST 21-AUG-2001
DEFINITION 603169877F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5249395 5', mRNA sequence.
ACCESSION BI452668
VERSION BI452668.1 GI:15243324
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 831)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11629 row: j column: 20
High quality sequence stop: 818.
FEATURES Location/Qualifiers
source 1. .831
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5249395"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"

/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
BASE COUNT 207 a 220 c 189 g 215 t
ORIGIN

Query Match 24.2%; Score 105.2; DB 12; Length 831;
Best Local Similarity 65.1%; Pred. No. 9.6e-19;
Matches 155; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

```
Qy         98 GTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCC 157
Db          2 GTGGTTGAAGGACAACCAACCACTGGATGCCAAAGATGTCAACCCCGAGAAGGTGCTACC 61

Qy        158 CAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCA 217
Db         62 TAACGGGGATGAGACCTATCAAGGCTGGCTGACATTGGCCGTGGCCCCTGGGGACGAGAC 121

Qy        218 GAGATATACGTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGG 277
Db        122 AAGGTTCACCTGTCAAGTGGAGCACCCAGGCCTGGACCAGCCTCTCACTGCCTCTTGGGA 181

Qy        278 TATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCC 335
Db        182 GCCCTTGCAATCTCAGGCCATGATTATTGGAATCATCAGTGGGGTCACCATCTGTGCC 239
```

RESULT 11
CB469137/c
LOCUS CB469137 611 bp mRNA linear EST 26-MAR-2003
DEFINITION sn03_F06.f sn Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CB469137
VERSION CB469137.1 GI:29275522
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 611)
AUTHORS Neilan,J.G., Kutish,G.F., Lu,Z., Zsak,A. and Rock,D.L.
TITLE Sequence analysis of African swine fever virus infected and non-infected porcine macrophage cDNA libraries
JOURNAL Unpublished
COMMENT Contact: Neilan JG
Plum Island Animal Disease Center
US Department of Agriculture, Agricultural Research Service
PO Box 848, Greenport, NY 11944-848, USA
Tel: 631 323 3133
Fax: 631 323 3044
Email: jneilan@piadc.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified by cross_match v0.990329 and lucy v1.17p.
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .611
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="lymphoid"
/cell_type="macrophage"
/lab_host="DH10B"
/clone_lib="sn"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Library made from pools of polyA selected RNA, isolated at different times post-infection (0 to 16 hrs) from African swine fever virus (isolate Pretorisuskop/96/4) infected swine macrophages. Macrophages were derived from peripheral blood mononuclear cells cultured for 48 hrs on plastic in the presence of 30% L929 supernatant."
BASE COUNT 133 a 171 c 163 g 144 t
ORIGIN

Query Match 20.3%; Score 88; DB 14; Length 611;
Best Local Similarity 61.7%; Pred. No. 6.1e-14;
Matches 158; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

```
Qy         47 CACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAA 106
Db        609 CACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTAAGGAGATCTCCCTGACCTGGCGGCG 550

Qy        107 GGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGA 166
Db        549 GGAGGGGCAGG---ACCAGAGCCAGGACGTGGAGGTTGTGGAAACCAGGCCCTCAGGGGA 493

Qy        167 TGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATAC 226
Db        492 TGGGACCTTCCAGAAGTGGGCGGCCCTGGTGGTGCCTCCTGGAGAGGAGCAGAGCTACAC 433

Qy        227 GTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACT 286
Db        432 CTGCCATGTGAAGCACGAGGGCCTGCAGGAGCCACTCACCCTGAGATGGGAACCGTCTCG 373

Qy        287 GATGAGAGCCAGGAGC 302
Db        372 GCTGTCCGCCATCACC 357
```

RESULT 12
CD245388
LOCUS CD245388 877 bp mRNA linear EST 22-MAY-2003
DEFINITION AGENCOURT_14098873 NIH_MGC_181 Homo sapiens cDNA clone IMAGE:30376798 5', mRNA sequence.
ACCESSION CD245388
VERSION CD245388.1 GI:31005852
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM439 row: p column: 23
High quality sequence stop: 693.
FEATURES Location/Qualifiers
source 1. .877
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30376798"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_181"
/note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
BASE COUNT 174 a 237 c 272 g 193 t 1 others
ORIGIN

```
  Query Match            20.3%;  Score 88;  DB 14;  Length 877;
  Best Local Similarity  63.3%;  Pred. No. 7e-14;
  Matches  152;  Conservative    0;  Mismatches   85;  Indels    3;  Gaps    1;

Qy         42 GTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGG 101
              | | |||| ||  ||||  ||||| ||  || ||||||   | | |||||  |||  |||
Db         10 GAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGG 69

Qy        102 CTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAAT 161
              | |  ||||  | ||     |  || ||||   ||| | |   ||     |||
Db         70 CAGCGGGATGGGGAGGA---CCAGACCCAGGACACCGAGCTTGTGGAGACCAGGCCAGCA 126

Qy        162 GGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGA 221
              || ||||| |||| ||||   |||  | |  |||  || ||  ||||  ||||||||||
Db        127 GGAGATGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCTGGACAAGAGCAGAGA 186

Qy        222 TATACGTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATG 281
              || ||||||||  || ||||   || ||| |  |||||||||  ||| |||||||| |
Db        187 TACACGTGCCATATGCAGCACGAGGGGCTGCAAGAGCCCCTCACCCTGAGCTGGGGTAAG 246


RESULT 13
BE487497
LOCUS       BE487497                490 bp    mRNA    linear   EST 27-MAR-2003
DEFINITION  176270 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE487497
VERSION     BE487497.1  GI:9607030
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P., Connor,E.E.
            , Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D. and
            Quackenbush,J.
  TITLE     Analysis of bovine mammary gland EST and functional annotation of
            the Bos taurus gene index
  JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
  MEDLINE   22135956
   PUBMED   12140684
COMMENT     Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@lpsi.barc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 138  row: G  column: 4
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="BARC 5BOV"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled mRNA isolated from mammary
                     tissues at eight physiological, developmental, and disease
                     states."
BASE COUNT      100 a    139 c    166 g     85 t
ORIGIN

  Query Match            20.0%;  Score 86.6;  DB 10;  Length 490;
  Best Local Similarity  62.1%;  Pred. No. 1.4e-13;
  Matches  172;  Conservative    0;  Mismatches   99;  Indels    6;  Gaps    2;

Qy          3 CCTCCTTTGGTGAAGGTGACACATCATGTGACCTCT---TCAGTGACCACTCTACGGTGT 59
              |||||  |||   | |||||  |||||     | ||||       | | -|||  ||  ||||
Db        170 CCTCCAATGGCACATGTGACCCATCACCCCAGCTCTGAGCGTGAGGTCACCCTGAGGTGC 229

Qy         60 CGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCA 119
              |||||  ||  || ||||||  || | ||| |  |||  ||||  |  ||  | ||
Db        230 TGGGCCCTGGGCTTCTACCCTAAGGAGATCTCACTGACCTGGCAGCGCGAGGGGGAG--- 286

Qy        120 ATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAG 179
                 |  || ||||  | || | |   ||       |||    |||||||| |||| ||||
Db        287 GACCAGACCCAGGACATGGAGCTTGTGGAGACCAGGCCTTCAGGGGATGGAACCTTCCAG 346

Qy        180 GGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAG 239
              |||  | || |||  || ||  |||| || |||||||||| |||||||| ||| ||
Db        347 AAGTGGGCAGCCCTGGTGGTGCCTTCTGGAGAGGAGCAGAGATACACGTGCCATGTGCAG 406

Qy        240 CACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 276
              |||  ||| ||  |  ||||||||||  |||  ||||
Db        407 CACGAAGGGCTTCAGGAGCCCCTCATCCTGAGATGGG 443


RESULT 14
AB005947
LOCUS       AB005947                752 bp    DNA     linear   GSS 04-AUG-1997
DEFINITION  Mouse genomic DNA, chromosome 17, clone cosmid 12.1, genomic survey
            sequence.
ACCESSION   AB005947
VERSION     AB005947.1  GI:2309033
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Yoshino,M., Jones,E. and Fischer Lindahl,K.
  TITLE     BAC clones from the H2-T region of the 129 mouse, Tlaf
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 752)
  AUTHORS   Yoshino,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUL-1997) Masayasu Yoshino, U.T. Southwestern Medical
            Center, HHMI; 5323 Harry Hines Blvd, Dallas, TX 75235-9050, USA
            (E-mail:YOSHINO@UTSW.SWMED.EDU, Tel:214-648-5047, Fax:214-648-5453)
FEATURES             Location/Qualifiers
     source          1. .752
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
                     /chromosome="17"
                     /clone="cosmid 12.1"
                     /haplotype="H2d"
                     /note="primer pTL5'(5'-cgcttccatcagcgtttatag)"
BASE COUNT      161 a    196 c    198 g    192 t      5 others
ORIGIN

  Query Match            19.9%;  Score 86.2;  DB 29;  Length 752;
  Best Local Similarity  63.4%;  Pred. No. 2.1e-13;
  Matches  149;  Conservative    0;  Mismatches   83;  Indels    3;  Gaps    1;

Qy         47 CACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAA 106
              ||| ||  ||||  |||||  ||  ||  ||| ||      || |||||  |||  |||| |||
Db        186 CACCCTGAGGTGCTGGGCCCTGGGCTTCTATCCTGCTGACCTCACCCTGACCTGGCAGAA 245

Qy        107 GGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGA 166
              ||||  | ||    ||    || ||||  | ||   | |||       |||    |||||
Db        246 GGATGGGGAGGAGCTGA---CCCAGGACATGGAGTTTGTAGAGACCAGGCCTGCAGGGGA 302

Qy        167 TGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATAC 226
              ||| |||| ||||   |||  | |  |||  || || | |||| ||||||||||  || ||
```

```
Db        303 TGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTCTTGGGAAAGAGCAGAGTTACAC 362

Qy        227 GTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATG 281
              ||||| ||| | ||    || |||  | |||||||||   |||  |||||||| |
Db        363 ATGCCATGTGTACCATGAGGGGCTGCCTGAGCCCCTCACCCTGAGATGGGGTAAG 417


RESULT 15
BM694948
LOCUS       BM694948                467 bp    mRNA    linear   EST 28-FEB-2002
DEFINITION  UI-E-CI1-afr-j-06-0-UI.r1 UI-E-CI1 Homo sapiens cDNA clone
            UI-E-CI1-afr-j-06-0-UI 5', mRNA sequence.
ACCESSION   BM694948
VERSION     BM694948.1  GI:19008206
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 467)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .467
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-CI1-afr-j-06-0-UI"
                     /tissue_type="RPE and Choroid"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-CI1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-CI1 is a normalized cDNA library containing the
                     following tissue(s): RPE and Choroid. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is ACCTA.
                     This library was created for the program, Gene Discovery
                     in the Visual System, supported by National Eye Institute
                     (NEI)."
BASE COUNT       92 a    143 c    149 g     83 t
ORIGIN

  Query Match             19.6%;  Score 85.2;  DB 12;  Length 467;
  Best Local Similarity   60.9%;  Pred. No. 3.4e-13;
  Matches  157;  Conservative    0;  Mismatches   98;  Indels    3;  Gaps    1;

Qy         24 CATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAG 83
              ||||  ||  |        | | ||||  ||  ||||  |||||  ||  ||  ||||||    |
Db         33 CATCCCGTCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCG 92

Qy         84 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 143
              | |||||  |||  ||||  |  ||||     ||         |  |  ||||   |||  | |
Db         93 GAGATCACACTGACCTGGCAGCGGGATGGCGAG---GACCAAACTCAGGACACCGAGCTT 149

Qy        144 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 203
                ||      |||    || |||||  |||| ||||   |||  |  |  |||  || ||
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Qy        204 CCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTC 263
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Qy        264 ATTGTGATCTGGGGTATG 281
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Db        270 ACCCTGAGATGGGGTAAG 287


Search completed: February 11, 2004, 17:10:55
Job time : 1746.84 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 14:07:35 ; Search time 225.083 Seconds
(without alignments)
5204.994 Million cell updates/sec

Title: US-09-981-606-27_COPY_6494_6927
Perfect score: 434
Sequence: 1 tgcctcctttggtgaaggtg.....acttgctttttctgttttag 434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	434	100.0	12146	21	AAA96794	Genomic DNA of a h
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	3	432.4	99.6	5749	25	ABX59735	cDNA encoding nove
	4	432.4	99.6	10825	18	AAT96690	Hereditary haemoch
	5	432.4	99.6	10825	22	AAC68425	Human hereditary h
	6	432.4	99.6	10825	22	AAC68427	Human hereditary h
c	7	432.4	99.6	235033	19	AAV57926	Hereditary haemoch
	8	430.8	99.3	10825	22	AAC68426	Human hereditary h
	9	430.8	99.3	10825	22	AAC68428	Human hereditary h
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	11	416.4	95.9	517	22	AAC68440	Human hereditary h
	12	414.8	95.6	517	22	AAC68441	Human hereditary h
	13	329	75.8	359	20	AAX16055	Hereditary hemochr
	14	277	63.8	1317	24	ABK49917	DNA encoding beta
	15	276	63.6	1440	18	AAT96691	Hereditary haemoch
	16	276	63.6	1440	22	AAC68429	Human hereditary h
	17	276	63.6	1440	22	AAC68431	Human hereditary h
	18	276	63.6	2506	21	AAA96769	cDNA sequence enco
	19	276	63.6	2727	19	AAV23525	Haemochromatosis g
	20	274.4	63.2	1440	22	AAC68430	Human hereditary h
	21	274.4	63.2	1440	22	AAC68432	Human hereditary h
	22	93	21.4	100	22	AAH02415	Human HLA-H exon 4
	23	91.4	21.1	100	22	AAH02416	Human HLA-H exon 4
	24	88	20.3	3098	22	ABA18125	Human nervous syst
	25	88	20.3	3098	22	AAS40421	DNA encoding human
	26	88	20.3	3098	22	AAL04024	Human reproductive
	27	88	20.3	3098	22	AAK86871	Human immune/haema
c	28	88	20.3	148834	24	ABK83570	Human cDNA differe
	29	86.4	19.9	4316	22	ABA83122	HLA-Cw ovarian tum
	30	86.4	19.9	4316	24	ABN97218	Gene #3716 used to
	31	85.2	19.6	3372	22	AAI63979	Human polynucleoti
	32	85.2	19.6	3372	22	AAI64011	Human polynucleoti
	33	84.6	19.5	2034	23	AAS90913	DNA encoding novel
	34	84.6	19.5	2037	23	AAS90740	DNA encoding novel
c	35	83.6	19.3	305	22	ABA51289	Human breast cell
c	36	83.6	19.3	305	22	ABA69295	Human foetal liver
c	37	83.6	19.3	305	22	ABA36224	Probe #14690 for g
c	38	83.6	19.3	305	22	AAK17581	Human brain expres
c	39	83.6	19.3	305	22	AAK43395	Human bone marrow
c	40	83.6	19.3	305	22	AAI24176	Probe #14109 for g
c	41	83.6	19.3	305	22	AAI49463	Probe #18149 used
c	42	83.6	19.3	305	22	AAI09738	Probe #9729 used t
c	43	83.6	19.3	305	23	ABS43016	Human liver single
c	44	83.6	19.3	305	24	ABS17488	Human genome-deriv
	45	83.6	19.3	321	24	ABL64433	Stomach cancer rel

ALIGNMENTS

RESULT 1
AAA96794
ID AAA96794 standard; cDNA; 12146 BP.
XX
AC AAA96794;
XX
DT 19-FEB-2001 (first entry)
XX
DE Genomic DNA of a histocompatibility iron loading (HFE) gene.
XX
KW Human; histocompatibility iron loading protein; HFE protein;
KW major histocompatibility complex; non-classical class I gene;
KW chromosome 6p; iron disorder; haemochromatosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 1028..1324
FT /*tag= a
FT /number= 1
FT intron 1325..4651
FT /*tag= b
FT /number= 1
FT exon 4652..4915
FT /*tag= c
FT /number= 2
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FT   exon            10206..10637
FT                   /*tag=  m
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PN   WO200058515-A1.
XX
PD   05-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US07982.
XX
PR   26-MAR-1999;   99US-0277457.
XX
PA   (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI   Rothenberg BE,  Sawada-Hirai R,  Barton JC;
XX
DR   WPI; 2000-647244/62.
XX
PT   Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT   susceptibility to develop it, by determining the presence of a mutation
PT   in exon 2 or an intron of a histocompatibility iron loading nucleic
PT   acid -
XX
PS   Example 1; Page 21-28; 55pp; English.
XX
CC   The present sequence represents the human histocompatibility iron
CC   loading (HFE) gene. The HFE gene is a major histocompatibility (MHC)
CC   non-classical class I gene located on chromosome 6p. Mutations in the
CC   gene lead to iron disorders. The specification describes a method for
CC   diagnosing an iron disorder or a genetic susceptibility to develop the
CC   disorder in a mammal. The method comprises determining the presence of
CC   a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
CC   is not a C to G missense mutation at nucleotide 187 of the sequence
CC   given in A96769 (Genbank Accession number U60319). The presence of the
CC   mutation indicates the disorder or the genetic susceptibility to the
CC   disorder. The method is used to diagnose an iron disorder
CC   e.g. haemochromatosis, or a genetic susceptibility to develop it.
XX
SQ   Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 other;

  Query Match             100.0%;  Score 434;  DB 21;  Length 12146;
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  Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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RESULT 2
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ID   AAL36747 standard; DNA; 5749 BP.
XX
AC   AAL36747;
XX
DT   08-JAN-2002  (first entry)
XX
DE   Human musculoskeletal system related polynucleotide SEQ ID NO 3112.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein;
KW   musculoskeletal system; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155367-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01338.
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PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
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PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-451937/48.
XX
PT Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -
XX
PS Example 2; SEQ ID NO 3112; 781pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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XX
SQ   Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;

  Query Match             99.6%;  Score 432.4;  DB 22;  Length 5749;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-121;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1605 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 1664

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       1665 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 1724

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db       2025 TTTTTCTGTTTTAG 2038


RESULT 3
ABX59735
ID   ABX59735 standard; cDNA; 5749 BP.
XX
AC   ABX59735;
XX
DT   26-FEB-2003  (first entry)
XX
DE   cDNA encoding novel human musculoskeletal system antigen #2079.
XX
KW   Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW   re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KW   cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW   post-operative tissue repair; limb regeneration; neuronal growth;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   AIDS-related complex; chondrocyte growth; bone regeneration;
KW   periodontal regeneration; tissue transport; bone graft; skin aging;
KW   keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW   cell growth; organ transplant; cell differentiation; body height;
KW   weight; hair colour; eye colour; skin; percentage of adipose tissue;
KW   pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm;
KW   depression; tendency for violence; pain; reproductive capability;
KW   hormone level; endocrine level; appetite; libido; memory; stress;
KW   storage capability; fat content; lipid content; protein content;
KW   carbohydrate content; vitamin content; cofactor content;
KW   nutritional component.
XX
OS   Homo sapiens.
XX
PN   US2002147140-A1.
XX
PD   10-OCT-2002.
XX
PF   17-JAN-2001; 2001US-0764877.
XX
PR   31-JAN-2000; 2000US-179065P.
PR   04-FEB-2000; 2000US-180628P.
PR   28-JUN-2000; 2000US-214886P.
PR   07-JUL-2000; 2000US-216647P.
PR   07-JUL-2000; 2000US-216880P.
PR   11-JUL-2000; 2000US-217487P.
PR   11-JUL-2000; 2000US-217496P.
PR   14-JUL-2000; 2000US-218290P.
PR   26-JUL-2000; 2000US-220963P.
PR   26-JUL-2000; 2000US-220964P.
PR   14-AUG-2000; 2000US-224518P.
PR   14-AUG-2000; 2000US-224519P.
PR   14-AUG-2000; 2000US-225267P.
PR   14-AUG-2000; 2000US-225268P.
PR   14-AUG-2000; 2000US-225270P.
PR   14-AUG-2000; 2000US-225447P.
PR   14-AUG-2000; 2000US-225757P.
PR   14-AUG-2000; 2000US-225758P.
PR   22-AUG-2000; 2000US-226868P.
PR   30-AUG-2000; 2000US-228924P.
PR   01-SEP-2000; 2000US-229287P.
PR   01-SEP-2000; 2000US-229343P.
PR   01-SEP-2000; 2000US-229344P.
PR   01-SEP-2000; 2000US-229345P.
PR   05-SEP-2000; 2000US-229509P.
PR   05-SEP-2000; 2000US-229513P.
PR   08-SEP-2000; 2000US-231413P.
PR   21-SEP-2000; 2000US-234223P.
PR   21-SEP-2000; 2000US-234274P.
PR   25-SEP-2000; 2000US-234997P.
PR   27-SEP-2000; 2000US-235834P.
PR   29-SEP-2000; 2000US-236327P.
PR   29-SEP-2000; 2000US-236367P.
PR   29-SEP-2000; 2000US-236368P.
PR   29-SEP-2000; 2000US-236369P.
PR   29-SEP-2000; 2000US-236370P.
PR   02-OCT-2000; 2000US-236802P.
PR   02-OCT-2000; 2000US-237037P.
PR   02-OCT-2000; 2000US-237038P.
PR   02-OCT-2000; 2000US-237039P.
PR   02-OCT-2000; 2000US-237040P.
PR   13-OCT-2000; 2000US-239935P.
PR   20-OCT-2000; 2000US-240960P.
PR   20-OCT-2000; 2000US-241785P.
PR   20-OCT-2000; 2000US-241809P.
PR   01-NOV-2000; 2000US-244617P.
PR   17-NOV-2000; 2000US-249299P.
PR   08-DEC-2000; 2000US-251856P.
PR   08-DEC-2000; 2000US-251868P.
PR   08-DEC-2000; 2000US-251869P.
XX
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
XX
PI   Rosen CA,  Ruben SM,  Barash SC;
XX
DR   WPI; 2003-128199/12.
XX
PT   Isolated nucleic acid molecules encoding musculoskeletal system
PT   associated polypeptides, useful for detecting disorders, e.g. cancer -
XX
PS   Disclosure; SEQ ID NO 3112; 321pp; English.
XX
CC   The invention describes an isolated nucleic acid molecule comprising a
CC   sequence encoding musculoskeletal system associated polypeptides useful
CC   for detecting disorders, e.g., cancer or cancer metastases, in animals
CC   or humans. The nucleic acid: stimulates re-vascularisation of ischaemic
CC   tissues associated with conditions such as thrombosis, arteriosclerosis,
CC   and other cardiovascular conditions; treats wounds due to injuries,
CC   burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
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CC   and limb regeneration; stimulates neuronal growth; can treat and prevent
CC   neuronal damage occurring in certain disorders or neurodegenerative
CC   conditions, such as, Alzheimer's disease, Parkinson's disease, and
CC   AIDS-related complex; stimulates chondrocyte growth, thus they can be
CC   used to enhance bone and periodontal regeneration and aid in tissue
CC   transports or bone grafts; prevents skin aging due to sunburn by
CC   stimulating keratinocyte growth; prevents hair loss, since FGF family
CC   members activate hair-forming cells and promotes melanocyte growth;
CC   stimulates growth and differentiation of hematopoietic cells and bone
CC   marrow cells when used in combination with other cytokines; maintains
CC   organs before transplantation or for supporting cell culture of primary
CC   tissues; induces tissue of mesodermal origin to differentiate in early
CC   embryos; increases or decreases the differentiation or proliferation of
CC   embryonic stem cells, besides, haematopoietic lineage; modulates
CC   mammalian characteristics, such as, body height, weight, hair colour, eye
CC   colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC   (e.g., cosmetic surgery); modulates mammalian metabolism; changes
CC   mammal's metal state or physical state by influencing biorhythms,
CC   caricadic rhythms, depression, tendency for violence, tolerance for pain,
CC   reproductive capabilities, hormonal or endocrine levels, appetite,
CC   libido, memory, or stress; increases or decreases storage capabilities,
CC   fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC   or other nutritional components. This sequence encodes a novel human
CC   musculoskeletal system antigen.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from the US patent office at
CC   ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140.
XX
SQ   Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;

  Query Match             99.6%;  Score 432.4;  DB 25;  Length 5749;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-121;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1605 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 1664

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1665 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 1724

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1725 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1784

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1785 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1844

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1845 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 1904

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1905 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 1964

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1965 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 2024

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       2025 TTTTTCTGTTTTAG 2038


RESULT 4
AAT96690
ID   AAT96690 standard; DNA; 10825 BP.
XX
AC   AAT96690;
XX
DT   14-APR-1998  (first entry)
XX
DE   Hereditary haemochromatosis gene.
XX
KW   Hereditary haemochromatosis; metal toxicity; diagnosis;
KW   gene therapy; prenatal screening; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             361..7147
FT                   /*tag=  a
FT                   /note= "contains introns"
FT   intron          437..3761
FT                   /*tag=  b
FT                   /number= 1
FT   intron          4026..4234
FT                   /*tag=  c
FT                   /number= 2
FT   intron          4511..5605
FT                   /*tag=  d
FT                   /number= 3
FT   intron          5882..6039
FT                   /*tag=  e
FT                   /number= 4
FT   intron          6154..7106
FT                   /*tag=  f
FT                   /number= 5
FT   mutation        3872
FT                   /*tag=  g
FT                   /note= "C to G substitution (24d2 mutation)
FT                         results in His to Asp substitution"
FT   variation       3878
FT                   /*tag=  h
FT                   /note= "A to T substitution (24d7 variant)
FT                         results in Ser to Cys substitution"
FT   mutation        5834
FT                   /*tag=  i
FT                   /note= "G to A substitution (24d1 mutation
FT                         associated with HH), results in Cys to
FT                         Tyr substitution"
XX
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US06254.
XX
PR   23-MAY-1996;   96US-0652265.
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   P-PSDB; AAW36499.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis
PT   and treatment of hereditary haemochromatosis disease
XX
PS   Disclosure; Fig 3; 115pp; English.
XX
CC   This genomic DNA sequence corresponds to the human gene whose
CC   mutated form is associated with hereditary haemochromatosis (HH).
CC   To identify this novel gene, allelic association patterns were
CC   determined between known markers and the HH locus in the HLA region
CC   of chromosome 6.  A physical clone coverage was then generated
CC   extending from D6S265, which is a marker that is centromeric of
CC   HLA-A, in a telomeric direction through D6S276, a marker at which
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CC   the allelic association was no longer observed.  A single mutation
CC   (24d1) in the HH gene appears responsible for the majority of HH
CC   disease.  This comprises a G to A substitution that is present in
CC   86% of affected chromosomes and in 4% of unaffected chromosomes.
CC   It results in a Cys to Tyr substitution in the encoded protein (see
CC   AAW36499) at a critical disulphide bridge important for secondary
CC   structure.  The following are claimed: the HH genomic DNA (I), a
CC   1437 bp cDNA sequence (Ia) (see AAT96691) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a
CC   peptide product chosen from the HH gene product, its variants
CC   (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC   residues of these; an antibody produced using the peptide; a method
CC   to determine the presence or absence of the common HH gene
CC   mutation; an animal model for the HH disease; metal chelation
CC   agents, T-cell differentiation factors and therapeutic agents for
CC   the mitigation of injury due to oxidative process in vivo or
CC   mitigation of iron overload; a method for screening potential
CC   therapeutic agents for activity in connection with HH disease; an
CC   antisense oligonucleotide directed against a transcriptional
CC   product of a nucleic acid sequence as above; and oligonucleotides
CC   or pairs of oligonucleotides covering a range of nucleotides from
CC   (I), (Ia) or their variants, useful for detecting a polymorphism in
CC   the HH gene.  The invention also relates to methods for screening
CC   for HH homozygotes, to HH diagnosis, prenatal screening and
CC   diagnosis, and therapies of HH disease, including gene therapy,
CC   protein- and antibody-based therapeutics, and small molecule
CC   therapeutics.
XX
SQ   Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;

  Query Match             99.6%;  Score 432.4;  DB 18;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 3.5e-121;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039


RESULT 5
AAC68425
ID   AAC68425 standard; DNA; 10825 BP.
XX
AC   AAC68425;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
DR   P-PSDB; AAB36869.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 3; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;

  Query Match             99.6%;  Score 432.4;  DB 22;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 3.5e-121;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025
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Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039
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RESULT 6
AAC68427
ID   AAC68427 standard; DNA; 10825 BP.
XX
AC   AAC68427;
XX
DT   21-FEB-2001 (first entry)
XX
DE   Human hereditary hemochromatosis 24d2 mutation DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA) BIO-RAD LAB INC.
XX
PI   Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
DR   P-PSDB; AAB36871.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 3; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 other;

  Query Match   99.6%; Score 432.4; DB 22; Length 10825;
  Best Local Similarity   99.8%; Pred. No. 3.5e-121;
  Matches 433; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039
```

RESULT 7
AAV57926/c
ID   AAV57926 standard; DNA; 235033 BP.
XX
AC   AAV57926;
XX
DT   23-DEC-1998 (first entry)
XX
DE   Hereditary haemochromatosis subregion from an unaffected individual.
XX
KW   Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW   diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW   BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW   type 1 sodium transport gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO9814466-A1.
XX
PD   09-APR-1998.
XX
PF   30-SEP-1997;   97WO-US17658.
XX
PR   07-MAY-1997;   97US-0852495.
PR   01-OCT-1996;   96US-0724394.
XX
PA   (PROG-) PROGENTIOR INC.
XX
PI   Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;
PI   Tsuchihashi Z, Wolff RK;
XX
DR   WPI; 1998-240014/21.
XX
PT   Hereditary haemochromatosis gene products - used to develop products
PT   for the diagnosis and treatment of hereditary disorders in iron
PT   metabolism
XX
PS   Example 2; Fig 8; 209pp; English.
XX
CC   The present invention describes hereditary haemochromatosis gene
CC   products from the human haemochromatosis gene. The present sequence
CC   represents a hereditary haemochromatosis subregion from an individual
CC   unaffected by hereditary haemochromatosis (HH). Also described is a
CC   method to determine the presence or absence of the common hereditary
CC   haemochromatosis (HFE) gene mutation in an individual comprising:
CC   (a) providing DNA or RNA from the individual; and (b) assessing the
CC   DNA or RNA for the presence or absence of a haplotype or genotype where
CC   the presence or absence of the haplotype genotype indicates the likely
CC   presence of the HFE gene mutation in the genome of the individual. The
CC   HFE gene sequences from the present invention can be used to develop
CC   products for use in the diagnosis and treatment of HFE. The present
CC   invention also describes BTF genes, which are homologues of the milk
CC   protein butyrophilin (BT), and can be used in the production of agonists
CC   and antagonists of BT function. Also described are: (1) a RoRet gene
CC   which can be used to develop products for the study, diagnosis and

```
CC   treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC   which are homologues of a type 1 sodium transport gene, and can
CC   similarly be used for hypophosphatemia.
XX
SQ   Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;

  Query Match             99.6%;  Score 432.4;  DB 19;  Length 235033;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-120;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41544 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 41485

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41484 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 41425

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41424 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 41365

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41364 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 41305

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41304 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 41245

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41244 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 41185

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      41184 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 41125

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db      41124 TTTTTCTGTTTTAG 41111


RESULT 8
AAC68426
ID   AAC68426 standard; DNA; 10825 BP.
XX
AC   AAC68426;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d1 mutation DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
DR   P-PSDB; AAB36870.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 3; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;

  Query Match             99.3%;  Score 430.8;  DB 22;  Length 10825;
  Best Local Similarity   99.5%;  Pred. No. 1.1e-120;
  Matches  432;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039


RESULT 9
AAC68428
ID   AAC68428 standard; DNA; 10825 BP.
XX
AC   AAC68428;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d1/2 mutation DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
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XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
DR   P-PSDB; AAB36872.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 3; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 other;

  Query Match             99.3%;  Score 430.8;  DB 22;  Length 10825;
  Best Local Similarity   99.5%;  Pred. No. 1.1e-120;
  Matches  432;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039


RESULT 10
AAV57903/c
ID   AAV57903 standard; DNA; 237326 BP.
XX
AC   AAV57903;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Hereditary haemochromatosis subregion from an HH affected individual.
XX
KW   Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW   diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW   BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW   type 1 sodium transport gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO9814466-A1.
XX
PD   09-APR-1998.
XX
PF   30-SEP-1997;   97WO-US17658.
XX
PR   07-MAY-1997;   97US-0852495.
PR   01-OCT-1996;   96US-0724394.
XX
PA   (PROG-) PROGENTIOR INC.
XX
PI   Feder JN,  Kronmal GS,  Lauer PM,  Ruddy DA,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1998-240014/21.
XX
PT   Hereditary haemochromatosis gene products - used to develop products
PT   for the diagnosis and treatment of hereditary disorders in iron
PT   metabolism
XX
PS   Claim 1; Fig 9; 209pp; English.
XX
CC   The present invention describes hereditary haemochromatosis gene
CC   products from the human haemochromatosis gene. The present sequence
CC   represents a hereditary haemochromatosis subregion from an hereditary
CC   haemochromatosis (HH) affected individual. Also described is a
CC   method to determine the presence or absence of the common hereditary
CC   haemochromatosis (HFE) gene mutation in an individual comprising:
CC   (a) providing DNA or RNA from the individual; and (b) assessing the
CC   DNA or RNA for the presence or absence of a haplotype or genotype where
CC   the presence or absence of the haplotype genotype indicates the likely
CC   presence of the HFE gene mutation in the genome of the individual. The
CC   HFE gene sequences from the present invention can be used to develop
CC   products for use in the diagnosis and treatment of HFE. The present
CC   invention also describes BTF genes, which are homologues of the milk
CC   protein butyrophilin (BT), and can be used in the production of agonists
CC   and antagonists of BT function. Also described are: (1) a RoRet gene
CC   which can be used to develop products for the study, diagnosis and
CC   treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC   which are homologues of a type 1 sodium transport gene, and can
CC   similarly be used for hypophosphatemia.
XX
SQ   Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;

  Query Match             98.9%;  Score 429.2;  DB 19;  Length 237326;
  Best Local Similarity   99.3%;  Pred. No. 1.1e-119;
  Matches  431;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41496 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 41437

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41436 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 41377

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      41376 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACGAGG 41317

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
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Db      41316 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 41257

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41256 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 41197

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41196 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 41137

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      41136 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 41077

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db      41076 TTTTTCTGTTTTAG 41063


RESULT 11
AAC68440
ID   AAC68440 standard; DNA; 517 BP.
XX
AC   AAC68440;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis DNA used for mutation detection.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 6; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 517 BP; 126 A; 120 C; 147 G; 124 T; 0 other;

  Query Match             95.9%;  Score 416.4;  DB 22;  Length 517;
  Best Local Similarity   99.8%;  Pred. No. 8.4e-117;
  Matches  417;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 159

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 219

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 279

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 339

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 399

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 459

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTT 418
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        460 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTT 517


RESULT 12
AAC68441
ID   AAC68441 standard; DNA; 517 BP.
XX
AC   AAC68441;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis DNA used for mutation detection.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 6; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 517 BP; 127 A; 120 C; 146 G; 124 T; 0 other;
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  Query Match             95.6%;  Score 414.8;  DB 22;  Length 517;
  Best Local Similarity   99.5%;  Pred. No. 2.6e-116;
  Matches  416;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 159

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 219

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 279

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 339

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 399

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 459

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTT 418
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        460 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTT 517
```

RESULT 13
AAX16055
ID AAX16055 standard; DNA; 359 BP.
XX
AC AAX16055;
XX
DT 19-MAY-1999 (first entry)
XX
DE Hereditary hemochromatosis gene target nucleic acid sequence.
XX
KW Hereditary hemochromatosis gene; encapsulate; lipoprotein outer membrane;
KW membrane stability; test cell; molecular diagnosis; genetic testing; ss.
XX
OS Unidentified.
XX
PN WO9906594-A1.
XX
PD 11-FEB-1999.
XX
PF 29-JUL-1998; 98WO-US15641.
XX
PR 23-DEC-1997; 97US-0997522.
PR 31-JUL-1997; 97US-0905124.
XX
PA (MAIN-) MAINE MEDICAL CENT.
XX
PI Rundell CA, Vary CPH;
XX
DR WPI; 1999-153816/13.
XX
PT Biological preparation of a stably encapsulated reference nucleic
PT acid - useful for molecular diagnostic and genetic testing
XX
PS Claim 5; Page 48; 51pp; English.
XX
CC The present sequence represents a nucleic acid sequence that is used as
CC a reference sequence to exemplify the method of the invention. The
CC specification describes a method for the biological preparation of a
CC stably encapsulated reference nucleic acid for molecular diagnostic and
CC genetic testing. The method comprises inserting a vector containing a
CC reference nucleic acid into a cell through its lipoprotein outer membrane
CC to encapsulate the nucleic acid, multiplying the cell to propagate the
CC nucleic acid, inducing cell death without affecting the nucleic acid,
CC and achieving a desired stability of the cell membrane for substantially
CC matching the nucleic acid with the membrane stability of test cells. The
CC reference nucleic acids are useful for molecular diagnosis and genetic
CC testing.
XX
SQ Sequence 359 BP; 86 A; 91 C; 101 G; 81 T; 0 other;

```
  Query Match             75.8%;  Score 329;  DB 20;  Length 359;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-90;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 90

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 150

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 210

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 270

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 330

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGG 329
              |||||||||||||||||||||||||||||
Db        331 GCTGAGAAAATCTATTGGGGGTTGAGAGG 359
```

RESULT 14
ABK49917
ID ABK49917 standard; cDNA; 1317 BP.
XX
AC ABK49917;
XX
DT 15-JUL-2002 (first entry)
XX
DE DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
XX
KW Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
KW iron absorption regulator; intracellular iron absorption; lung injury;
KW haemochromatosis; transfusion; thalassaemia; haemolytic anaemia;
KW chronic infection; transferrin receptor; TfR; brain tumour; cancer;
KW oxidative stress disorder; tissue damage; vascular disease;
KW inflammation; atherosclerosis; autoimmune disease;
KW inflammatory condition; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..1317
FT   /*tag= a
FT   /product= "beta2M/HFE monochain"
XX
PN WO200224929-A2.
XX
PD 28-MAR-2002.
XX
PF 24-SEP-2001; 2001WO-US29873.
XX
PR 22-SEP-2000; 2000US-234843P.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

```
PA   (MCIN/) MCINNIS P.
XX
PI   Ehrlich R,  Rotem-Yehudar R,  Laham N;
XX
DR   WPI; 2002-383192/41.
DR   P-PSDB; AAU80035.
XX
PT   Soluble beta 2 microglobulin/HFE monochain useful for treating
PT   iron-overload conditions e.g. thalassemia and chronic infections,
PT   comprises human beta 2 microglobulin linked to alpha domains of HFE by
PT   a linker peptide  -
XX
PS   Example 2; Fig 2; 77pp; English.
XX
CC   The invention relates to a soluble polypeptide (I) of beta 2
CC   microglobulin (beta2m)/HFE monochain comprising human beta2m (or its
CC   analogue or active fragment), linked to alpha1-alpha3 domains of human
CC   HFE (a central regulator of iron absorption; undefined), or its analogue
CC   or active fragment, by a flexible linker peptide, or a functional
CC   derivative or salt of (I). (I) is useful for reducing intracellular iron
CC   absorption in patients having hereditary haemochromatosis, transfusions,
CC   thalassaemias, haemolytic anaemia or chronic infections, and for
CC   delivering a therapeutic to cells that over-express transferrin receptor
CC   (TfR) which are preferably lymphocytes or leukocytes, across the blood-
CC   brain barrier. (I) is further useful for treating brain tumour. (I)
CC   is also useful for treating oxidative stress disorders resulting in
CC   tissue damage e.g. vascular diseases, inflammation, atherosclerosis,
CC   lung injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful
CC   as a platform for drug delivery of therapeutic use for cancer,
CC   autoimmune diseases and inflammatory conditions. The monochain manifests
CC   specific characteristics advantageous for drug delivery systems. It is a
CC   soluble, stable and fully conformed protein. It binds specifically to
CC   transferrin receptor (TfR) and therefore targets cells that over-express
CC   this receptor. It is continuously internalised by the target cells, thus
CC   enabling efficient drug delivery. It dissociates from the receptor in the
CC   cells, minimising side effects. It negatively regulates iron absorption,
CC   reducing growth of undesired cells and preventing lymphocyte activation.
CC   It is not diluted in the blood as is transferrin. It should not induce an
CC   immune response since it is a self non-polymeric protein and delivery of
CC   drugs via monochain is expected to overcome drug-resistance since it is a
CC   natural TfR-binding protein. The present sequence represents the
CC   coding sequence of beta2m/HFE monochain.
XX
SQ   Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;

  Query Match             63.8%;  Score 277;  DB 24;  Length 1317;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-74;
  Matches  277;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db        953 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 1012

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 1072

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       1073 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1132

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1133 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1192

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGG 277
              |||||||||||||||||||||||||||||||||||||
Db       1193 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGG 1229


RESULT 15
AAT96691
ID   AAT96691 standard; cDNA; 1440 BP.
XX
AC   AAT96691;
XX
DT   14-APR-1998  (first entry)
XX
DE   Hereditary haemochromatosis gene cDNA clone.
XX
KW   Hereditary haemochromatosis; metal toxicity; diagnosis;
KW   gene therapy; prenatal screening; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             222.1268
FT                   /*tag=  a
FT   mutation        408
FT                   /*tag=  g
FT                   /note= "C to G substitution (24d2 mutation)
FT                          results in His to Asp substitution"
FT   variation       414
FT                   /*tag=  h
FT                   /note= "A to T substitution (24d7 variant)
FT                          results in Ser to Cys substitution"
FT   mutation        1066
FT                   /*tag=  i
FT                   /note= "G to A substitution (24d1 mutation
FT                          associated with HH), results in Cys to
FT                          Tyr substitution"
XX
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US06254.
XX
PR   23-MAY-1996;   96US-0652265.
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   P-PSDB; AAW36499.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis
PT   and treatment of hereditary haemochromatosis disease
XX
PS   Disclosure; Fig 4; 115pp; English.
XX
CC   This cDNA clone, designated cDNA24, is derived from human gene
CC   whose mutated form is associated with hereditary haemochromatosis
CC   (HH).  It was obtained from a directionally cloned plasmid-based
CC   cDNA library following identification of the HH locus in the HLA
CC   region of chromosome 6.  A single mutation (24d1) in the HH gene
CC   appears responsible for the majority of HH disease.  This comprises
CC   a G to A substitution that is present in 86% of affected
CC   chromosomes and in 4% of unaffected chromosomes.  It results in a
CC   Cys to Tyr substitution in the encoded protein (see AAW36499) at a
CC   critical disulphide bridge important for secondary structure.  The
CC   following are claimed: a 10825 bp genomic DNA sequence (I) (see
CC   AAT96690), the 1437 bp cDNA sequence (Ia) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a
CC   peptide product chosen from the HH gene product, its variants
CC   (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC   residues of these; an antibody produced using the peptide; a method
CC   to determine the presence or absence of the common HH gene
CC   mutation; an animal model for the HH disease; metal chelation
CC   agents, T-cell differentiation factors and therapeutic agents for
CC   the mitigation of injury due to oxidative process in vivo or
CC   mitigation of iron overload; a method for screening potential
```

CC therapeutic agents for activity in connection with HH disease; an
CC antisense oligonucleotide directed against a transcriptional
CC product of a nucleic acid sequence as above; and oligonucleotides
CC or pairs of oligonucleotides covering a range of nucleotides from
CC (I), (Ia) or their variants, useful for detecting a polymorphism in
CC the HH gene. The invention also relates to methods for screening
CC for HH homozygotes, to HH diagnosis, prenatal screening and
CC diagnosis, and therapies of HH disease, including gene therapy,
CC protein- and antibody-based therapeutics, and small molecule
CC therapeutics.
XX
SQ Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

Query Match 63.6%; Score 276; DB 18; Length 1440;
Best Local Similarity 100.0%; Pred. No. 7.9e-74;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 897

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 957

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1017

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1077

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 276
              ||||||||||||||||||||||||||||||||||||
Db       1078 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 1113
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Search completed: February 11, 2004, 15:27:03
Job time : 226.083 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 16:24:07 ; Search time 272.96 Seconds
(without alignments)
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Title: US-09-981-606-27_COPY_6494_6927
Perfect score: 434
Sequence: 1 tgcctcctttggtgaaggtg.....acttgctttttctgttttag 434

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Searched: 2449703 seqs, 1841816367 residues

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SUMMARIES

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	2	432.4	99.6	5749	10	US-09-764-877-3112	Sequence 3112, Ap
	3	432.4	99.6	5749	12	US-10-242-515-3112	Sequence 3112, Ap
	4	432.4	99.6	10825	13	US-10-138-888-1	GENERAL INFORMA
	5	432.4	99.6	10825	13	US-10-138-888-5	GENERAL INFORMA
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	15	276	63.6	1440	13	US-10-138-888-77	Sequence 77, Appl
	16	276	63.6	2506	13	US-09-981-606-1	Sequence 1, Appli
	17	274.4	63.2	1440	13	US-10-138-888-10	Sequence 10, Appl
	18	274.4	63.2	1440	13	US-10-138-888-12	Sequence 12, Appl
	19	93	21.4	100	13	US-10-272-665-112	Sequence 112, App
	20	93	21.4	100	13	US-10-273-321-112	Sequence 112, App
	21	93	21.4	100	13	US-10-272-756-112	Sequence 112, App
	22	93	21.4	100	13	US-10-273-228-112	Sequence 112, App
	23	91.4	21.1	100	13	US-10-272-665-113	Sequence 113, App
	24	91.4	21.1	100	13	US-10-273-321-113	Sequence 113, App
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	26	91.4	21.1	100	13	US-10-273-228-113	Sequence 113, App
	27	88	20.3	289	13	US-10-029-386-18154	Sequence 18154, A
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	35	85.2	19.6	3372	12	US-10-158-057-383	Sequence 383, App
c	36	83.6	19.3	301	13	US-10-029-386-19081	Sequence 19081, A
c	37	83.6	19.3	305	9	US-09-864-761-21544	Sequence 21544, A
	38	83.6	19.3	321	9	US-09-962-436-311	Sequence 311, App
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	42	81.8	18.8	276	13	US-10-029-386-18770	Sequence 18770, A
	43	81.8	18.8	484	11	US-09-918-995-32571	Sequence 32571, A
	44	81.8	18.8	1210	13	US-10-093-463-77	Sequence 77, Appl
	45	81.8	18.8	1377	14	US-10-044-090-563	Sequence 563, App

ALIGNMENTS

RESULT 1
US-09-981-606-27
; Sequence 27, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg et al.
; TITLE OF INVENTION: Mutations associated with iron disorders
; FILE REFERENCE: 24065-004CON
; CURRENT APPLICATION NUMBER: US/09/981,606
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 12146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-606-27

Query Match 100.0%; Score 434; DB 13; Length 12146;
Best Local Similarity 100.0%; Pred. No. 8.3e-139;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       6494 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 6553

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       6554 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 6613

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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 6733

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6734 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 6793

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6794 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 6853

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6854 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6913

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6914 TTTTTCTGTTTTAG 6927


RESULT 2
US-09-764-877-3112
; Sequence 3112, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC005
;  CURRENT APPLICATION NUMBER: US/09/764,877
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 4031
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3112
;   LENGTH: 5749
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1222)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-764-877-3112

  Query Match             99.6%;  Score 432.4;  DB 10;  Length 5749;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-138;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db       2025 TTTTTCTGTTTTAG 2038


RESULT 3
US-10-242-515-3112
; Sequence 3112, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC005C1
;  CURRENT APPLICATION NUMBER: US/10/242,515
;  CURRENT FILING DATE:  2002-09-13
;  PRIOR APPLICATION NUMBER: 09/764,877
;  PRIOR FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: 60/179,065
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/180,628
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: 60/214,886
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/217,487
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,758
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/220,963
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/217,496
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,447
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/218,290
;  PRIOR FILING DATE: 2000-07-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4031
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3112
;   LENGTH: 5749
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1222)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-242-515-3112

  Query Match             99.6%;  Score 432.4;  DB 12;  Length 5749;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-138;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       1725 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1784

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1785 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1844

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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db       2025 TTTTTCTGTTTTAG 2038
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RESULT 4
US-10-138-888-1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;             OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;             (HH) protein"
;             /note= "No. US20030148972A1mal or wild-type (unaffected)
;             Hereditary Hemochromatosis (HH) gene
;             allele"
;        FEATURE:
;             NAME/KEY:  -
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;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  5507..6023
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(3878, "a")
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;             (unaffected)"
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;             /label= 24d1
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-138-888-1

  Query Match             99.6%;  Score 432.4;  DB 13;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-138;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Qy        421 TTTTTCTGTTTTAG 434
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RESULT 5
US-10-138-888-5
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
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;               FILING DATE: 02-May-2002
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: US 08/834,497
;               FILING DATE: 04-APR-1997
;               APPLICATION NUMBER: US 08/652,265
;               FILING DATE: 23-MAY-1996
;               APPLICATION NUMBER: US 08/632,673
;               FILING DATE: 16-APR-1996
;               APPLICATION NUMBER: US 08/630,912
;               FILING DATE: 04-APR-1996
;          ATTORNEY/AGENT INFORMATION:
;               NAME: Brian M. Poissant
;               REGISTRATION NUMBER: 28,462
;               REFERENCE/DOCKET NUMBER: 8907-095-999
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (212) 790-9090
;               TELEFAX: (212) 869-8864
;               OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;               (HH) protein containing the 24d2
;               mutation"
;               /note= "Hereditary Hemochromatosis (HH)
;               gene 24d2 allele"
;          FEATURE:
;               NAME/KEY:  -
;               LOCATION:  140..7319
;          FEATURE:
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;               LOCATION:  5507..6023
;          SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-138-888-5

  Query Match             99.6%;  Score 432.4;  DB 13;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-138;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

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Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 6
US-10-138-888-79
;  GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;            OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;            (HH) protein containing the 24d7 mutation"
;            /note= "Hereditary Hemochromatosis
;            (HH)gene 24d7 allele"
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  140..7319
;       FEATURE:
;            NAME/KEY:  -
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;            LOCATION:  replace(3878, "t")
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;            /label= 24d7
;       SEQUENCE DESCRIPTION: SEQ ID NO: 79:
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  Query Match             99.6%;  Score 432.4;  DB 13;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-138;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

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Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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RESULT 7
US-10-301-844-1/c
; Sequence 1, Application US/10301844
; Publication No. US20030100747A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruddy, David A.
;                   Wolff, Roger K.
;        TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
;                            HEMOCHROMATOSIS GENE
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds, LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/301,844
;             FILING DATE: 20-No. US20030100747A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/852,495C
;             FILING DATE: 07-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-0057-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;    INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 235033 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-301-844-1

  Query Match             99.6%;  Score 432.4;  DB 15;  Length 235033;
  Best Local Similarity   99.8%;  Pred. No. 1e-137;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41544 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 41485

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41484 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 41425

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41424 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 41365

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41364 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 41305

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41304 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 41245

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41244 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 41185

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      41184 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 41125

Qy        421 TTTTTCTGTTTTAG 434
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Db      41124 TTTTTCTGTTTTAG 41111
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RESULT 8
US-10-138-888-3
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;
```

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;           REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 790-9090
;           TELEFAX: (212) 869-8864
;           OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;           (HH) protein containing the 24d1
;           mutation"
;           /note= "Hereditary Hemochromatosis (HH)
;           gene 24d1 allele"
;       FEATURE:
;           NAME/KEY:  -
;           LOCATION:  140..7319
;       FEATURE:
;           NAME/KEY:  -
;           LOCATION:  5507..6023
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-138-888-3

  Query Match             99.3%;  Score 430.8;  DB 13;  Length 10825;
  Best Local Similarity   99.5%;  Pred. No. 1e-137;
  Matches  432;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039


RESULT 9
US-10-138-888-7
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Pennie & Edmonds LLP
;           STREET: 1155 Avenue of the Americas
;           CITY: New York
;           STATE: New York
;           COUNTRY: USA
;           ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/138,888
;           FILING DATE: 02-May-2002
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/834,497
;           FILING DATE: 04-APR-1997
;           APPLICATION NUMBER: US 08/652,265
;           FILING DATE: 23-MAY-1996
;           APPLICATION NUMBER: US 08/632,673
;           FILING DATE: 16-APR-1996
;           APPLICATION NUMBER: US 08/630,912
;           FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Brian M. Poissant
;           REGISTRATION NUMBER: 28,462
;           REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 790-9090
;           TELEFAX: (212) 869-8864
;           OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;           (HH) protein containing both the 24d1
;           and 24d2 mutations"
;           /note= "Hereditary Hemochromatosis (HH)
;           gene containing a combination of both
;           24d1 and 24d2 alleles"
;       FEATURE:
;           NAME/KEY:  -
;           LOCATION:  140..7319
;       FEATURE:
;           NAME/KEY:  -
;           LOCATION:  5507..6023
;       FEATURE:
;           NAME/KEY:  allele
;           LOCATION:  replace(5834, "a")
;           OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;           (HH)"
;           /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-138-888-7

  Query Match             99.3%;  Score 430.8;  DB 13;  Length 10825;
  Best Local Similarity   99.5%;  Pred. No. 1e-137;
  Matches  432;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039


RESULT 10
US-10-301-844-2/c
; Sequence 2, Application US/10301844
; Publication No. US20030100747A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruddy, David A.
;                   Wolff, Roger K.
;        TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
;                            HEMOCHROMATOSIS GENE
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds, LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/301,844
;             FILING DATE: 20-No. US20030100747A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/852,495C
;             FILING DATE: 07-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-0057-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 237326 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-301-844-2

  Query Match             99.3%;  Score 430.8;  DB 15;  Length 237326;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-137;
  Matches  432;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41496 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 41437

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41436 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 41377

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db      41376 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 41317

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db      41316 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 41257

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db      41256 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 41197

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db      41196 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 41137

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
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Qy        421 TTTTTCTGTTTTAG 434
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Db      41076 TTTTTCTGTTTTAG 41063


RESULT 11
US-10-138-888-20
; Sequence 20, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 20:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 517 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
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;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..517
;            OTHER INFORMATION:  /note= "normal or wild-type (unaffected)
;            genomic sequence surrounding variant for
;            24d1(G) allele corresponding to positions
;            5507-6023 of genomic sequence containing
;            the HH gene (SEQ ID NO:1)"
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(328, "g")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-138-888-20

  Query Match             95.9%;  Score 416.4;  DB 13;  Length 517;
  Best Local Similarity   99.8%;  Pred. No. 2.6e-133;
  Matches  417;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 159

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 219

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 279

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 339

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 399

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 459

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTT 418
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        460 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTT 517


RESULT 12
US-10-138-888-21
; Sequence 21, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 517 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..517
;            OTHER INFORMATION:  /note= "genomic sequence surrounding
;            variant for 24d1(A) allele corresponding
;            to positions 5507-6023 of genomic
;            sequence containing the HH gene
;            (SEQ ID NO:3)"
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(328, "a")
;            OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;            (HH)"
;            /label= 24d1
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-138-888-21

  Query Match             95.6%;  Score 414.8;  DB 13;  Length 517;
  Best Local Similarity   99.5%;  Pred. No. 9.4e-133;
  Matches  416;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 159

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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RESULT 13
US-10-138-888-9
; Sequence 9, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1440 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  222..1268
;        FEATURE:
;             NAME/KEY:  allele
;             LOCATION:  replace(408, "c")
;             OTHER INFORMATION:  /phenotype= "normal or wild-type
;             (unaffected)"
;             /label= 24d2
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;             LOCATION:  replace(414, "a")
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US-10-138-888-9

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US-10-138-888-11
; Sequence 11, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
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;              FILING DATE: 16-APR-1996
;              APPLICATION NUMBER: US 08/630,912
;              FILING DATE: 04-APR-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Brian M. Poissant
;              REGISTRATION NUMBER: 28,462
;              REFERENCE/DOCKET NUMBER: 8907-095-999
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212) 790-9090
;              TELEFAX: (212) 869-8864
;    INFORMATION FOR SEQ ID NO: 11:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1440 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         FEATURE:
;              NAME/KEY:  CDS
;              LOCATION:  222..1268
;         FEATURE:
;              NAME/KEY:  allele
;              LOCATION:  replace(408, "g")
;              OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;              (HH)"
;              /label= 24d2
;         SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-138-888-11

  Query Match             63.6%;  Score 276;  DB 13;  Length 1440;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-84;
  Matches  276;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        838 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 897

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       1078 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 1113


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; Sequence 77, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;         APPLICANT: Thomas, Winston J.
;                    Drayna, Dennis T.
;                    Feder, John N.
;                    Gnirke, Andreas
;                    Ruddy, David
;                    Tsuchihashi, Zenta
;                    Wolff, Roger K.
;         TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;         NUMBER OF SEQUENCES: 79
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Pennie & Edmonds LLP
;              STREET: 1155 Avenue of the Americas
;              CITY: New York
;              STATE: New York
;              COUNTRY: USA
;              ZIP: 10036-2711
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
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;              FILING DATE: 02-May-2002
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/834,497
;              FILING DATE: 04-APR-1997
;              APPLICATION NUMBER: US 08/652,265
;              FILING DATE: 23-MAY-1996
;              APPLICATION NUMBER: US 08/632,673
;              FILING DATE: 16-APR-1996
;              APPLICATION NUMBER: US 08/630,912
;              FILING DATE: 04-APR-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Brian M. Poissant
;              REGISTRATION NUMBER: 28,462
;              REFERENCE/DOCKET NUMBER: 8907-095-999
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212) 790-9090
;              TELEFAX: (212) 869-8864
;    INFORMATION FOR SEQ ID NO: 77:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1440 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         FEATURE:
;              NAME/KEY:  CDS
;              LOCATION:  222..1268
;         FEATURE:
;              NAME/KEY:  allele
;              LOCATION:  replace(414, "t")
;              OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;              (HH)"
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;         SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-138-888-77

  Query Match             63.6%;  Score 276;  DB 13;  Length 1440;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-84;
  Matches  276;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db        838 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 897

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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       1018 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1077

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 276
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Db       1078 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 1113


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GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	434	100.0	12146	21	US-09-439-378A-1	Sequence 1, Appli
3	434	100.0	12146	43	US-09-981-606-27	Sequence 27, Appl
4	432.4	99.6	2555	32	US-09-724-676-18070	Sequence 18070, A

	5	432.4	99.6	2555	32	US-09-724-676A-18070 Sequence 18070, A
	6	432.4	99.6	2819	32	US-09-724-676-18073 Sequence 18073, A
	7	432.4	99.6	2819	32	US-09-724-676A-18073 Sequence 18073, A
	8	432.4	99.6	5749	1	PCT-US01-01338-3112 Sequence 3112, Ap
	9	432.4	99.6	5749	2	PCT-US01-01338-3112 Sequence 3112, Ap
	10	432.4	99.6	5749	33	US-09-764-877-3112 Sequence 3112, Ap
	11	432.4	99.6	5749	48	US-10-242-515-3112 Sequence 3112, Ap
	12	432.4	99.6	10825	13	US-08-834-497-1 Sequence 1, Appli
	13	432.4	99.6	10825	13	US-08-834-497-5 Sequence 5, Appli
	14	432.4	99.6	10825	21	US-09-497-957-1 Sequence 1, Appli
	15	432.4	99.6	10825	21	US-09-497-957-5 Sequence 5, Appli
	16	432.4	99.6	10825	46	US-10-138-888-1 GENERAL INFORMA
	17	432.4	99.6	10825	46	US-10-138-888-5 GENERAL INFORMA
	18	432.4	99.6	10825	46	US-10-138-888-79 GENERAL INFORMA
	19	432.4	99.6	13607	40	US-09-949-016-11806 Sequence 11806, A
	20	432.4	99.6	13609	40	US-09-949-016-12922 Sequence 12922, A
c	21	432.4	99.6	235033	13	US-08-852-495A-1 Sequence 1, Appli
c	22	432.4	99.6	235033	13	US-08-852-495C-1 Sequence 1, Appli
c	23	432.4	99.6	235033	50	US-10-301-844-1 Sequence 1, Appli
	24	432	99.5	21608	101	US-60-465-241-51931 Sequence 51931, A
	25	432	99.5	21608	101	US-60-466-412-85138 Sequence 85138, A
	26	430.8	99.3	10825	13	US-08-834-497-3 Sequence 3, Appli
	27	430.8	99.3	10825	13	US-08-834-497-7 Sequence 7, Appli
	28	430.8	99.3	10825	21	US-09-497-957-3 Sequence 3, Appli
	29	430.8	99.3	10825	21	US-09-497-957-7 Sequence 7, Appli
	30	430.8	99.3	10825	46	US-10-138-888-3 GENERAL INFORMA
	31	430.8	99.3	10825	46	US-10-138-888-7 GENERAL INFORMA
c	32	430.8	99.3	237326	13	US-08-852-495A-2 Sequence 2, Appli
c	33	430.8	99.3	237326	13	US-08-852-495C-2 Sequence 2, Appli
c	34	430.8	99.3	237326	50	US-10-301-844-2 Sequence 2, Appli
	35	416.4	95.9	517	13	US-08-834-497-20 Sequence 20, Appl
	36	416.4	95.9	517	13	US-08-891-250-3 Sequence 3, Appli
	37	416.4	95.9	517	21	US-09-497-957-20 Sequence 20, Appl
	38	416.4	95.9	517	46	US-10-138-888-20 Sequence 20, Appl
	39	415.4	95.7	517	13	US-08-891-250-13 Sequence 13, Appl
	40	414.8	95.6	517	13	US-08-834-497-21 Sequence 21, Appl
	41	414.8	95.6	517	13	US-08-891-250-4 Sequence 4, Appli
	42	414.8	95.6	517	21	US-09-497-957-21 Sequence 21, Appl
	43	414.8	95.6	517	46	US-10-138-888-21 Sequence 21, Appl
	44	396.2	91.3	2513	32	US-09-724-676-18072 Sequence 18072, A
	45	396.2	91.3	2513	32	US-09-724-676A-18072 Sequence 18072, A

ALIGNMENTS

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RESULT 1
US-09-439-378-1
; Sequence 1, Application US/09439378
; GENERAL INFORMATION:
;  APPLICANT:  London Health Sciences Centre
;  TITLE OF INVENTION:  METHOD FOR DIAGNOSIS OF HEREDITARY HEMOCHROMATOSIS
;  FILE REFERENCE:  4767-98/PAR
;  CURRENT APPLICATION NUMBER: US/09/439,378
;  CURRENT FILING DATE:  1999-11-15
;  PRIOR APPLICATION NUMBER:  2,272,410
;  PRIOR FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 12146
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-439-378-1

  Query Match             100.0%;  Score 434;  DB 21;  Length 12146;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-117;
  Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6494 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 6553

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6554 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 6613

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 6673

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 6733

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6734 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 6793

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6794 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 6853

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6854 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6913

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6914 TTTTTCTGTTTTAG 6927


RESULT 2
US-09-439-378A-1
; Sequence 1, Application US/09439378A
; GENERAL INFORMATION:
;  APPLICANT: London Health Sciences Centre
;  TITLE OF INVENTION: METHOD FOR DIAGNOSIS OF HEREDITARY HEMOCHROMATOSIS
;  FILE REFERENCE: 4767-98/PAR
;  CURRENT APPLICATION NUMBER: US/09/439,378A
;  CURRENT FILING DATE:  1999-11-15
;  PRIOR APPLICATION NUMBER: 2,272,410
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 12146
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-439-378A-1

  Query Match             100.0%;  Score 434;  DB 21;  Length 12146;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-117;
  Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6494 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 6553

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6554 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 6613

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 6673

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 6733

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6734 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 6793

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       6794 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 6853

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6854 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6913

Qy        421 TTTTTCTGTTTTAG 434
                ||||||||||||||
Db       6914 TTTTTCTGTTTTAG 6927


RESULT 3
US-09-981-606-27
; Sequence 27, Application US/09981606
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg et al.
;  TITLE OF INVENTION: Mutations associated with iron disorders
;  FILE REFERENCE: 24065-004CON
;  CURRENT APPLICATION NUMBER: US/09/981,606
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 12146
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-981-606-27

  Query Match             100.0%;  Score 434;  DB 43;  Length 12146;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-117;
  Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6494 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 6553

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6554 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 6613

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 6673

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 6733

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6734 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 6793

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6794 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 6853

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6854 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6913

Qy        421 TTTTTCTGTTTTAG 434
                ||||||||||||||
Db       6914 TTTTTCTGTTTTAG 6927


RESULT 4
US-09-724-676-18070
; Sequence 18070, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18070
;   LENGTH: 2555
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676-18070

  Query Match             99.6%;  Score 432.4;  DB 32;  Length 2555;
  Best Local Similarity   99.8%;  Pred. No. 4.7e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 633

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 693

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 753

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 813

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 873

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 933

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
                ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        934 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 993

Qy        421 TTTTTCTGTTTTAG 434
                ||||||||||||||
Db        994 TTTTTCTGTTTTAG 1007


RESULT 5
US-09-724-676A-18070
; Sequence 18070, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18070
;   LENGTH: 2555
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676A-18070

  Query Match             99.6%;  Score 432.4;  DB 32;  Length 2555;
  Best Local Similarity   99.8%;  Pred. No. 4.7e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 633
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Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
Db        634 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 693

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
Db        694 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 753

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
Db        754 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 813

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
Db        814 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 873

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
Db        874 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 933

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
Db        934 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 993

Qy        421 TTTTTCTGTTTTAG 434
Db        994 TTTTTCTGTTTTAG 1007
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RESULT 6
US-09-724-676-18073
; Sequence 18073, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18073
; LENGTH: 2819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-18073

Query Match 99.6%; Score 432.4; DB 32; Length 2819;
Best Local Similarity 99.8%; Pred. No. 4.8e-117;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
Db        838 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 897

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
Db        898 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 957

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
Db        958 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1017

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
Db       1018 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1077

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
Db       1078 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 1137

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
Db       1138 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 1197

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
Db       1198 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 1257

Qy        421 TTTTTCTGTTTTAG 434
Db       1258 TTTTTCTGTTTTAG 1271
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RESULT 7
US-09-724-676A-18073
; Sequence 18073, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18073
; LENGTH: 2819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-18073

Query Match 99.6%; Score 432.4; DB 32; Length 2819;
Best Local Similarity 99.8%; Pred. No. 4.8e-117;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
Db        838 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 897

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
Db        898 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 957

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
Db        958 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1017

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
Db       1018 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1077

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
Db       1078 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 1137

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
Db       1138 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 1197

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
Db       1198 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 1257

Qy        421 TTTTTCTGTTTTAG 434
Db       1258 TTTTTCTGTTTTAG 1271
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RESULT 8
PCT-US01-01338-3112
; Sequence 3112, Application PC/TUS0101338
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01338

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;  CURRENT FILING DATE:  2001-01-14
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 4031
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3112
;   LENGTH: 5749
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1222)
;   OTHER INFORMATION: n equals a,t,g, or c
PCT-US01-01338-3112

  Query Match             99.6%;  Score 432.4;  DB 1;  Length 5749;
  Best Local Similarity   99.8%;  Pred. No. 6.2e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       1665 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 1724

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       1785 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1844

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       1965 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 2024

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       2025 TTTTTCTGTTTTAG 2038


RESULT 9
PCT-US01-01338-3112
; Sequence 3112, Application PC/TUS0101338
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc., et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC005PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/01338
;  CURRENT FILING DATE:  2001-01-14
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 4031
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3112
;   LENGTH: 5749
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1222)
;   OTHER INFORMATION: n equals a,t,g, or c
PCT-US01-01338-3112

  Query Match             99.6%;  Score 432.4;  DB 2;  Length 5749;
  Best Local Similarity   99.8%;  Pred. No. 6.2e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       1605 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 1664

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       1785 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1844

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       1845 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 1904

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       1965 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 2024

Qy        421 TTTTTCTGTTTTAG 434
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Db       2025 TTTTTCTGTTTTAG 2038


RESULT 10
US-09-764-877-3112
; Sequence 3112, Application US/09764877
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC005
;  CURRENT APPLICATION NUMBER: US/09/764,877
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 4031
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3112
;   LENGTH: 5749
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1222)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-764-877-3112

  Query Match             99.6%;  Score 432.4;  DB 33;  Length 5749;
  Best Local Similarity   99.8%;  Pred. No. 6.2e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1605 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 1664

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       1665 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 1724

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       1725 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1784

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Db       1785 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1844

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       1845 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 1904

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       1965 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 2024

Qy        421 TTTTTCTGTTTTAG 434
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Db       2025 TTTTTCTGTTTTAG 2038


RESULT 11
US-10-242-515-3112
; Sequence 3112, Application US/10242515
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC005C1
;  CURRENT APPLICATION NUMBER: US/10/242,515
;  CURRENT FILING DATE:  2002-09-13
;  PRIOR APPLICATION NUMBER: 09/764,877
;  PRIOR FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: 60/179,065
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/180,628
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: 60/214,886
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/217,487
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,758
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/220,963
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/217,496
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,447
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/218,290
;  PRIOR FILING DATE: 2000-07-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4031
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3112
;   LENGTH: 5749
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1222)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-242-515-3112

  Query Match             99.6%;  Score 432.4;  DB 48;  Length 5749;
  Best Local Similarity   99.8%;  Pred. No. 6.2e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1605 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 1664

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1725 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1784

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       1785 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1844

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       1845 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 1904

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       1965 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 2024

Qy        421 TTTTTCTGTTTTAG 434
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Db       2025 TTTTTCTGTTTTAG 2038


RESULT 12
US-08-834-497-1
; Sequence 1, Application US/08834497
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COJNTRY:  USA
;      ZIP:  94111-3834
;    COMPJTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
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;       REFERENCE/DOCKET NUMBER:  017957-000520US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 326-2400
;       TELEFAX:  (650) 326-2422
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10825 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;       LOCATION:  6040..6153, 7107..7147)
;       OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /note= "Normal or wild-type (unaffected)
;       OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;       OTHER INFORMATION:  allele"
;     FEATURE:
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;       OTHER INFORMATION:  normal or wild-type (unaffected) allele
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;       OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;       OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;       OTHER INFORMATION:  allele (SEQ ID NO:41)"
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;       OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
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US-08-834-497-1

  Query Match             99.6%;  Score 432.4;  DB 13;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 7.6e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 13
US-08-834-497-5
; Sequence 5, Application US/08834497
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000520US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 326-2400
;      TELEFAX:  (650) 326-2422
;  INFORMATION FOR SEQ ID NO:  5:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d2 allele"
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;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d2 allele cDNA (SEQ ID NO:11)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;    FEATURE:
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;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(G) allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-08-834-497-5

  Query Match             99.6%;  Score 432.4;  DB 13;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 7.6e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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; Sequence 1, Application US/09497957
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/497,957
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497
;      FILING DATE:  04-APR-1997
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
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;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= "Normal or wild-type (unaffected)
;      OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;      OTHER INFORMATION:  allele"
;    FEATURE:
;      NAME/KEY:  -
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;      OTHER INFORMATION:  normal or wild-type (unaffected) allele
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;       OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
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;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
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US-09-497-957-1

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  Best Local Similarity   99.8%;  Pred. No. 7.6e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


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; Sequence 5, Application US/09497957
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/497,957
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497
;      FILING DATE:  04-APR-1997
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
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;       LOCATION:  replace(3872, "g")
;       OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d2
US-09-497-957-5

  Query Match             99.6%;  Score 432.4;  DB 21;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 7.6e-117;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2004, 15:14:45 ; Search time 54.7163 Seconds
(without alignments)
3500.971 Million cell updates/sec

Title: US-09-981-606-27_COPY_6494_6927
Perfect score: 434
Sequence: 1 tgcctcctttggtgaaggtg.....acttgctttttctgttttag 434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	434	100.0	12146	4	US-09-277-457-27	Sequence 27, Appl
2	434	100.0	12146	4	US-09-679-729-27	Sequence 27, Appl
3	432.4	99.6	10825	3	US-08-652-265-1	Sequence 1, Appli
4	432.4	99.6	10825	3	US-08-652-265-5	Sequence 5, Appli
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6	432.4	99.6	10825	3	US-08-834-497A-5	Sequence 5, Appli
7	432.4	99.6	10825	3	US-09-503-444A-1	Sequence 1, Appli
8	432.4	99.6	10825	3	US-09-503-444A-5	Sequence 5, Appli
9	432.4	99.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
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11	432.4	99.6	246240	2	US-08-724-394A-22	Sequence 22, Appl
12	430.8	99.3	10825	3	US-08-652-265-3	Sequence 3, Appli
13	430.8	99.3	10825	3	US-08-652-265-7	Sequence 7, Appli
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38	274.4	63.2	1440	3	US-08-834-497A-10	Sequence 10, Appl
39	274.4	63.2	1440	3	US-08-834-497A-12	Sequence 12, Appl
40	274.4	63.2	1440	3	US-09-503-444A-10	Sequence 10, Appl
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42	84.6	19.5	1086	4	US-08-914-372C-2	Sequence 2, Appli
43	83	19.1	1086	4	US-08-914-372C-3	Sequence 3, Appli
44	83	19.1	1086	4	US-08-914-372C-35	Sequence 35, Appl
45	83	19.1	1095	4	US-08-914-372C-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-277-457-27
; Sequence 27, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Barry E.
; APPLICANT: Sawada-Hirai, Ritsuko
; APPLICANT: Barton, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERENCE: 10653/002001
; CURRENT APPLICATION NUMBER: US/09/277,457
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 12146
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-277-457-27

Query Match 100.0%; Score 434; DB 4; Length 12146;
Best Local Similarity 100.0%; Pred. No. 1.1e-141;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       6554 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 6613

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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       6854 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6913

Qy        421 TTTTTCTGTTTTAG 434
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Db       6914 TTTTTCTGTTTTAG 6927


RESULT 2
US-09-679-729-27
; Sequence 27, Application US/09679729
; Patent No. 6509442
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 24065-004 DIV
;  CURRENT APPLICATION NUMBER: US/09/679,729
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 12146
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-679-729-27

  Query Match             100.0%;  Score 434;  DB 4;  Length 12146;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-141;
  Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 6733

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db       6914 TTTTTCTGTTTTAG 6927


RESULT 3
US-08-652-265-1
; Sequence 1, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= "No. 6025130mal or wild-type (unaffected)
;      OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;      OTHER INFORMATION:  allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) allele
;      OTHER INFORMATION:  cDNA (SEQ ID NO:9)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;      OTHER INFORMATION:  allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
;      OTHER INFORMATION:  allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
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;       NAME/KEY:  allele
;       LOCATION:  replace(3878, "a")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d7
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;       NAME/KEY:  allele
;       LOCATION:  replace(5834, "g")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d1
US-08-652-265-1

  Query Match             99.6%;  Score 432.4;  DB 3;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-141;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       5846 ACCCAGGCCTGGATCAGCCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 4
US-08-652-265-5
; Sequence 5, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d2 allele"
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;      NAME/KEY:  -
;      LOCATION:  140..7319
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;      OTHER INFORMATION:  24d2 allele cDNA (SEQ ID NO:11)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(G) allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-08-652-265-5

  Query Match             99.6%;  Score 432.4;  DB 3;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-141;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 5
US-08-834-497A-1
; Sequence 1, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= "No. 6140305mal or wild-type (unaffected)
;      OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;      OTHER INFORMATION:  allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) allele
;      OTHER INFORMATION:  cDNA (SEQ ID NO:9)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;      OTHER INFORMATION:  allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
;      OTHER INFORMATION:  allele (SEQ ID NO:20)"
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;      NAME/KEY:  allele
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;      OTHER INFORMATION:  /phenotype= "normal or wild-type
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;      OTHER INFORMATION:  /phenotype= "normal or wild-type
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;      OTHER INFORMATION:  /label= 24d7
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;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-1

  Query Match             99.6%;  Score 432.4;  DB 3;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-141;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 6
US-08-834-497A-5
; Sequence 5, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d2 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d2 allele cDNA (SEQ ID NO:11)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(G) allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-08-834-497A-5

  Query Match             99.6%;  Score 432.4;  DB 3;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-141;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 7
US-09-503-444A-1
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; Sequence 1, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= "No. 6228594mal or wild-type (unaffected)
;      OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;      OTHER INFORMATION:  allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) allele
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;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;      OTHER INFORMATION:  allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
;      OTHER INFORMATION:  allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d2
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;      OTHER INFORMATION:  (unaffected)"
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;      OTHER INFORMATION:  /phenotype= "normal or wild-type
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;      OTHER INFORMATION:  /label= 24d1
US-09-503-444A-1

  Query Match             99.6%;  Score 432.4;  DB 3;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-141;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 8
US-09-503-444A-5
; Sequence 5, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
```

```
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d2 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d2 allele cDNA (SEQ ID NO:11)"
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;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
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;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(G) allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-09-503-444A-5

  Query Match             99.6%;  Score 432.4;  DB 3;  Length 10825;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-141;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 9
US-08-724-394A-20
; Sequence 20, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Kronmal, Gregory S.
;    APPLICANT:  Lauer, Peter M.
;    APPLICANT:  Ruddy, David A.
;    APPLICANT:  Thomas, Winston
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;    TITLE OF INVENTION:  Sequences and Antibodies Thereto
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,394A
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;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..246240
;      OTHER INFORMATION:  /note= "HLA-H.CONTIG"
US-08-724-394A-20

  Query Match             99.6%;  Score 432.4;  DB 2;  Length 246240;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-140;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db     197969 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 198028

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Db     198029 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 198088

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db     198089 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 198148

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Qy        421 TTTTTCTGTTTTAG 434
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RESULT 10
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; Sequence 21, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Kronmal, Gregory S.
;    APPLICANT:  Lauer, Peter M.
;    APPLICANT:  Ruddy, David A.
;    APPLICANT:  Thomas, Winston
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;    TITLE OF INVENTION:  Sequences and Antibodies Thereto
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,394A
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..246240
;      OTHER INFORMATION:  /note= "HLA-H.CONTIG"
US-08-724-394A-21

  Query Match             99.6%;  Score 432.4;  DB 2;  Length 246240;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-140;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197909 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 197968

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db     197969 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 198028

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db     198029 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 198088

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db     198089 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 198148

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db     198149 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 198208

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db     198209 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 198268

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db     198269 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 198328

Qy        421 TTTTTCTGTTTTAG 434
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Db     198329 TTTTTCTGTTTTAG 198342
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RESULT 11
US-08-724-394A-22
; Sequence 22, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Kronmal, Gregory S.
;    APPLICANT:  Lauer, Peter M.
;    APPLICANT:  Ruddy, David A.
;    APPLICANT:  Thomas, Winston
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;    TITLE OF INVENTION:  Sequences and Antibodies Thereto
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,394A
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..246240
;      OTHER INFORMATION:  /note= "HLA-H.CONTIG"
US-08-724-394A-22

  Query Match             99.6%;  Score 432.4;  DB 2;  Length 246240;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-140;
  Matches  433;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197909 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 197968

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197969 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 198028

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db     198029 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 198088

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db     198089 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 198148

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db     198149 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 198208

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198209 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 198268

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db     198269 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 198328

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db     198329 TTTTTCTGTTTTAG 198342


RESULT 12
US-08-652-265-3
; Sequence 3, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d1 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
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;       OTHER INFORMATION:  24d1 allele cDNA (SEQ ID NO:10)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  3852..3891
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d2(C) allele (SEQ ID NO:41)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  5507..6023
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(5834, "a")
;       OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d1
US-08-652-265-3

  Query Match             99.3%;  Score 430.8;  DB 3;  Length 10825;
  Best Local Similarity   99.5%;  Pred. No. 1.3e-140;
  Matches  432;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 13
US-08-652-265-7
; Sequence 7, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  and 24d2 mutations"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene containing a combination of both
;      OTHER INFORMATION:  24d1 and 24d2 alleles"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  cDNA containing a combination of both
;      OTHER INFORMATION:  24d1 and 24d2 alleles
;      OTHER INFORMATION:  (SEQ ID NO:12)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-7

  Query Match             99.3%;  Score 430.8;  DB 3;  Length 10825;
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  Best Local Similarity   99.5%;  Pred. No. 1.3e-140;
  Matches  432;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
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Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 14
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; Sequence 3, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d1 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d1 allele cDNA (SEQ ID NO:10)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(C) allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-3

  Query Match             99.3%;  Score 430.8;  DB 3;  Length 10825;
  Best Local Similarity   99.5%;  Pred. No. 1.3e-140;
  Matches  432;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
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Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 5845
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Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965

Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
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Qy        421 TTTTTCTGTTTTAG 434
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Db       6026 TTTTTCTGTTTTAG 6039


RESULT 15
US-08-834-497A-7
; Sequence 7, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  and 24d2 mutations"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene containing a combination of both
;      OTHER INFORMATION:  24d1 and 24d2 alleles"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  cDNA containing a combination of both
;      OTHER INFORMATION:  24d1 and 24d2 alleles
;      OTHER INFORMATION:  (SEQ ID NO:12)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "a")
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;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-7

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  Best Local Similarity   99.5%;  Pred. No. 1.3e-140;
  Matches  432;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60
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Db       5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665

Qy         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 5725

Qy        121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 180
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Db       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785

Qy        181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 5845

Qy        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905

Qy        301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965
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Qy        361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025

Qy        421 TTTTTCTGTTTTAG 434
              ||||||||||||||
Db       6026 TTTTTCTGTTTTAG 6039
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Search completed: February 11, 2004, 17:12:26
Job time : 56.7163 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 12, 2003, 21:53:18 ; Search time 109.119 Seconds
(without alignments)
6373.435 Million cell updates/sec

Title: US-09-981-606-30
Perfect score: 17
Sequence: 1 atcatgagtgtcgccgt 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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21: em_or:*
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23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		17	100.0	17	6	AR199266	AR199266 Sequence
2		17	100.0	17	6	AR275785	AR275785 Sequence
3		17	100.0	32	6	AR117826	AR117826 Sequence
4		17	100.0	32	6	AR149496	AR149496 Sequence
5		15.4	90.6	30	6	AX377053	AX377053 Sequence
6		15.4	90.6	31	6	AX393579	AX393579 Sequence
7		15.4	90.6	32	6	AR117825	AR117825 Sequence
8		15.4	90.6	32	6	AR149495	AR149495 Sequence
9		15.4	90.6	40	6	AR117823	AR117823 Sequence
10		15.4	90.6	40	6	AR149493	AR149493 Sequence
11		15.4	90.6	46	6	AX555611	AX555611 Sequence
12		15.4	90.6	46	6	AX598549	AX598549 Sequence
13	c	15.4	90.6	75	6	AX080199	AX080199 Sequence
14	c	15.4	90.6	76	6	AX080184	AX080184 Sequence
15		15.4	90.6	100	6	AX112462	AX112462 Sequence
16		15.4	90.6	735	9	AF115264	AF115264 Homo sapi
17		15.4	90.6	804	9	AF149804	AF149804 Homo sapi
18		15.4	90.6	874	9	HSHLAH2	Y09800 H.sapiens H
19		15.4	90.6	987	9	AF150664	AF150664 Homo sapi
20		15.4	90.6	1045	9	AF079407	AF079407 Homo sapi
21		15.4	90.6	1073	9	HSA249337	AJ249337 Homo sapi
22		15.4	90.6	1200	9	AF115265	AF115265 Homo sapi
23		15.4	90.6	1280	9	HSA249335	AJ249335 Homo sapi
24		15.4	90.6	1317	6	AX407339	AX407339 Sequence
25		15.4	90.6	1320	4	AY007543	AY007543 Dicerorhi
26		15.4	90.6	1440	6	AR117793	AR117793 Sequence
27		15.4	90.6	1440	6	AR117794	AR117794 Sequence
28		15.4	90.6	1440	6	AR149463	AR149463 Sequence
29		15.4	90.6	1440	6	AR149464	AR149464 Sequence
30		15.4	90.6	1486	10	MMU80604	U80604 Mus musculu
31	c	15.4	90.6	1515	6	I50840	I50840 Sequence 4
32		15.4	90.6	1529	10	MMU66849	U66849 Mus musculu
33		15.4	90.6	1885	9	AF144242	AF144242 Homo sapi
34		15.4	90.6	2506	6	AR199238	AR199238 Sequence
35		15.4	90.6	2506	6	AR275757	AR275757 Sequence
36		15.4	90.6	2727	9	HSU60319	U60319 Homo sapien
37		15.4	90.6	5982	6	AX701831	AX701831 Sequence
38	c	15.4	90.6	7742	6	I50838	I50838 Sequence 1
39	c	15.4	90.6	9342	1	BPETOXOP	L10720 Bordetella
40		15.4	90.6	10825	6	AR117789	AR117789 Sequence
41		15.4	90.6	10825	6	AR117790	AR117790 Sequence
42		15.4	90.6	10825	6	AR149459	AR149459 Sequence
43		15.4	90.6	10825	6	AR149460	AR149460 Sequence
44	c	15.4	90.6	11214	9	AF447807	AF447807 Pan trogl
45		15.4	90.6	12146	6	AR199263	AR199263 Sequence

ALIGNMENTS

RESULT 1
AR199266
LOCUS AR199266 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 30 from patent US 6355425.
ACCESSION AR199266
VERSION AR199266.1 GI:20249340
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.
TITLE Mutations associated with iron disorders
JOURNAL Patent: US 6355425-A 30 12-MAR-2002;
FEATURES Location/Qualifiers

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                     /organism="unknown"
BASE COUNT        3 a      4 c      5 g      5 t
ORIGIN

  Query Match             100.0%;  Score 17;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db          1 ATCATGAGTGTCGCCGT 17


RESULT 2
AR275785
LOCUS       AR275785                 17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 30 from patent US 6509442.
ACCESSION   AR275785
VERSION     AR275785.1  GI:29709342
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.
  TITLE     Mutations associated with iron disorders
  JOURNAL   Patent: US 6509442-A 30 21-JAN-2003;
FEATURES            Location/Qualifiers
     source         1. .17
                    /organism="unknown"
BASE COUNT        3 a      4 c      5 g      5 t
ORIGIN

  Query Match             100.0%;  Score 17;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db          1 ATCATGAGTGTCGCCGT 17


RESULT 3
AR117826
LOCUS       AR117826                 32 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 44 from patent US 6140305.
ACCESSION   AR117826
VERSION     AR117826.1  GI:14098732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 44 31-OCT-2000;
FEATURES            Location/Qualifiers
     source         1. .32
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BASE COUNT        5 a      5 c     11 g     11 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db         10 ATCATGAGTGTCGCCGT 26


RESULT 4
AR149496
LOCUS       AR149496                 32 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 44 from patent US 6228594.
ACCESSION   AR149496
VERSION     AR149496.1  GI:15114087
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 44 08-MAY-2001;
FEATURES            Location/Qualifiers
     source         1. .32
                    /organism="unknown"
BASE COUNT        5 a      5 c     11 g     11 t
ORIGIN

  Query Match             100.0%;  Score 17;  DB 6;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db         10 ATCATGAGTGTCGCCGT 26


RESULT 5
AX377053
LOCUS       AX377053                 30 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 11 from Patent WO0212557.
ACCESSION   AX377053
VERSION     AX377053.1  GI:19573347
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cailloux,F. and Gobron,S.
  TITLE     Method for detecting known mutations in tube
  JOURNAL   Patent: WO 0212557-A 11 14-FEB-2002;
            Nucleica (FR)
FEATURES            Location/Qualifiers
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /note="Detection de la mutation H63D dans le gene de
                    l'hemochromatose."
BASE COUNT        6 a      7 c     10 g      7 t
ORIGIN

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  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
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Db          5 ATCATGAGAGTCGCCGT 21


RESULT 6
AX393579
LOCUS       AX393579                 31 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 43 from Patent WO0214555.
ACCESSION   AX393579
VERSION     AX393579.1  GI:19701548
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wittwer,C.T., Crockett,A.O., Caplin,B.E., Stevenson,W.,
            Wagner,L.A., Chen,J. and Kusukawa,N.
  TITLE     Single-labeled oligonucleotide probes
  JOURNAL   Patent: WO 0214555-A 43 21-FEB-2002;
            University of Utah Research Foundation (US) ; Idaho Technology,
            Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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BASE COUNT        6 a      5 c     10 g     10 t
ORIGIN

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  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
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Db         10 ATCATGAGAGTCGCCGT 26


RESULT 7
AR117825
LOCUS       AR117825                  32 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 43 from patent US 6140305.
ACCESSION   AR117825
VERSION     AR117825.1  GI:14098731
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 43 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
BASE COUNT        6 a      5 c     11 g     10 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 6;  Length 32;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         10 ATCATGAGAGTCGCCGT 26


RESULT 8
AR149495
LOCUS       AR149495                  32 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 43 from patent US 6228594.
ACCESSION   AR149495
VERSION     AR149495.1  GI:15114086
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 43 08-MAY-2001;
FEATURES             Location/Qualifiers
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BASE COUNT        6 a      5 c     11 g     10 t
ORIGIN

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  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         10 ATCATGAGAGTCGCCGT 26


RESULT 9
AR117823
LOCUS       AR117823                  40 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 41 from patent US 6140305.
ACCESSION   AR117823
VERSION     AR117823.1  GI:14098729
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 41 31-OCT-2000;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db         19 ATCATGAGAGTCGCCGT 35


RESULT 10
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LOCUS       AR149493                  40 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 41 from patent US 6228594.
ACCESSION   AR149493
VERSION     AR149493.1  GI:15114084
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 41 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unknown"
BASE COUNT        7 a      7 c     13 g     13 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 6;  Length 40;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
```

```
              |||||||| ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 11
AX555611
LOCUS       AX555611                  46 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 207 from Patent WO02070755.
ACCESSION   AX555611
VERSION     AX555611.1  GI:25899104
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lyamichev,V.I., Kaiser,M.W. and Lyamicheva,N.
  TITLE     Fen endonucleases
  JOURNAL   Patent: WO 02070755-A 207 12-SEP-2002;
            Third Wave Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        7 a     11 c     15 g     13 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 6;  Length 46;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||| ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 12
AX598549
LOCUS       AX598549                  46 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 823 from Patent WO0244994.
ACCESSION   AX598549
VERSION     AX598549.1  GI:28398727
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brower,A., Brow,M.A., Cracauer,R.F., Fors,L., Granske,R., de arruda
            Indig,M., Kurensky,D., Luedtke,C., Lukowiak,A.A., Lyamichev,V.,
            Neri,B.P., Reimer,N.D., Roeven,R.T., Skrzypczynski,Z., Ziarno,W.A.,
            Comerford,J., Stump,S. and Viegut,D.D.
  TITLE     Systems and method for detection assay production and sale
  JOURNAL   Patent: WO 0244994-A 823 06-JUN-2002;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        7 a     11 c     15 g     13 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 6;  Length 46;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||| ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 13
AX080199/c
LOCUS       AX080199                  75 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 37 from Patent WO0107665.
ACCESSION   AX080199
VERSION     AX080199.1  GI:13159680
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Umek,R.M.
  TITLE     Sequence determination of nucleic acids using electronic detection
  JOURNAL   Patent: WO 0107665-A 37 01-FEB-2001;
            Clinical Micro Sensors, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .75
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic."
BASE COUNT       21 a     24 c     16 g     14 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 6;  Length 75;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||| ||||||||
Db         32 ATCATGAGAGTCGCCGT 16


RESULT 14
AX080184/c
LOCUS       AX080184                  76 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 22 from Patent WO0107665.
ACCESSION   AX080184
VERSION     AX080184.1  GI:13159665
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Umek,R.M.
  TITLE     Sequence determination of nucleic acids using electronic detection
  JOURNAL   Patent: WO 0107665-A 22 01-FEB-2001;
            Clinical Micro Sensors, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .76
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic."
BASE COUNT       21 a     24 c     17 g     14 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 6;  Length 76;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||| ||||||||
Db         32 ATCATGAGAGTCGCCGT 16


RESULT 15
AX112462
LOCUS       AX112462                 100 bp    DNA     linear   PAT 01-MAY-2001
DEFINITION  Sequence 110 from Patent WO0127857.
ACCESSION   AX112462
VERSION     AX112462.1  GI:13939221
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Braun,A., Koester,H., van den Boom,D., Ping,Y., Rodi,C., He,L.,
            Chiu,N. and Jurinke,C.
  TITLE     Methods for generating databases and databases for identifying
            polymorphic genetic markers
  JOURNAL   Patent: WO 0127857-A 110 19-APR-2001;
            Sequenom, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT       19 a     22 c     29 g     30 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 6;  Length 100;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||| |||||||||
Db         46 ATCATGAGAGTCGCCGT 62


Search completed: September 13, 2003, 00:51:37
Job time : 109.119 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 12, 2003, 18:58:38 ; Search time 13.0108 Seconds
(without alignments)
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Title: US-09-981-606-30
Perfect score: 17
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	100.0	17	21	AAA96797	Probe for detectin
	2	17	100.0	32	22	AAC68462	Sequence surroundi
	3	15.4	90.6	30	24	ABL56391	Gene fragment whic
	4	15.4	90.6	31	24	AAK98989	Human probe target
	5	15.4	90.6	32	22	AAC68461	Sequence surroundi
	6	15.4	90.6	40	22	AAC68459	Sequence surroundi
	7	15.4	90.6	47	22	AAH78015	DNA fragment with
c	8	15.4	90.6	75	22	AAF58246	Oligonucleotide D1
c	9	15.4	90.6	76	22	AAF58231	Oligonucleotide D1
	10	15.4	90.6	100	22	AAH02413	Human HLA-H exon 2
	11	15.4	90.6	596	22	AAI63897	Human polynucleoti
	12	15.4	90.6	1317	24	ABK49917	DNA encoding beta
	13	15.4	90.6	1440	18	AAT96691	Hereditary haemoch
	14	15.4	90.6	1440	22	AAC68429	Human hereditary h
	15	15.4	90.6	1440	22	AAC68430	Human hereditary h
	16	15.4	90.6	2506	21	AAA96769	cDNA sequence enco
	17	15.4	90.6	2727	19	AAV23525	Haemochromatosis g
	18	15.4	90.6	5982	25	ABV93934	Human colon specif
c	19	15.4	90.6	7742	18	AAT84745	Bordetella pertuss
	20	15.4	90.6	10825	18	AAT96690	Hereditary haemoch
	21	15.4	90.6	10825	22	AAC68425	Human hereditary h
	22	15.4	90.6	10825	22	AAC68426	Human hereditary h
	23	15.4	90.6	12146	21	AAA96794	Genomic DNA of a h
c	24	15.4	90.6	235033	19	AAV57926	Hereditary haemoch
c	25	15.4	90.6	237326	19	AAV57903	Hereditary haemoch
	26	14.4	84.7	20	22	AAH55966	Human SCN2A PCR-SS
c	27	14.4	84.7	234	25	ABZ41768	N. gonorrhoeae nuc
c	28	14.4	84.7	370	22	AAH55800	Human SCN2A genomi
	29	14.4	84.7	734	21	AAA82008	N. meningitidis pa
c	30	14.4	84.7	1791	24	ABK73785	Bacillus lichenifo
	31	14.4	84.7	1920	23	ABL08807	Drosophila melanog
c	32	14.4	84.7	4134	23	ABL08808	Drosophila melanog
c	33	14.4	84.7	8538	23	ABL08806	Drosophila melanog
c	34	14.4	84.7	349980	21	AAF21607	Neisseria meningit
c	35	14.4	84.7	1437668	21	AAA81490	N. meningitidis B
c	36	14	82.4	65	24	ABN29608	Rat spliced transc
c	37	14	82.4	375	24	ABK79755	Bacillus clausii g
c	38	14	82.4	9051	23	ABL03186	Drosophila melanog
c	39	14	82.4	129021	21	AAF22296	BAC containing rep
c	40	13.8	81.2	27	24	AAK98987	Human probe HHDP2
c	41	13.8	81.2	27	24	AAK98988	Human probe HHDP3
c	42	13.8	81.2	28	24	AAK98986	Human probe HHDP1
	43	13.8	81.2	30	24	ABL56392	Mutated gene fragm
	44	13.8	81.2	31	24	AAK98990	Human probe target
	45	13.8	81.2	40	22	AAC68460	Sequence surroundi

ALIGNMENTS

RESULT 1
AAA96797
ID AAA96797 standard; DNA; 17 BP.
XX
AC AAA96797;
XX
DT 19-FEB-2001 (first entry)
XX
DE Probe for detecting histocompatibility iron loading gene mutation S65C.
XX
KW Human; histocompatibility iron loading protein; HFE protein;
KW major histocompatibility complex; non-classical class I gene;
KW chromosome 6p; iron disorder; haemochromatosis; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200058515-A1.
XX
PD 05-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US07982.
XX
PR 26-MAR-1999; 99US-0277457.
XX
PA (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI Rothenberg BE, Sawada-Hirai R, Barton JC;
XX
DR WPI; 2000-647244/62.
XX
PT Diagnosing an iron disorder e.g. hemochromatosis or a genetic

PT susceptibility to develop it, by determining the presence of a mutation
PT in exon 2 or an intron of a histocompatibility iron loading nucleic
PT acid -
XX
PS Example 1; Page 29; 55pp; English.
XX
CC The present sequence represents a probe which is used to detect the
CC mutation S65C in the human histocompatibility iron loading (HFE)
CC protein. The HFE gene is a major histocompatibility (MHC) non-classical
CC class I gene located on chromosome 6p. Mutations in the gene lead to
CC iron disorders. The specification describes a method for diagnosing an
CC iron disorder or a genetic susceptibility to develop the disorder in a
CC mammal. The method comprises determining the presence of a mutation in
CC exon 2 or an intron of a HFE gene or protein. The mutation is not a C
CC to G missense mutation at nucleotide 187 of the sequence given in
CC A96769 (Genbank Accession number U60319). The presence of the mutation
CC indicates the disorder or the genetic susceptibility to the disorder. The
CC method is used to diagnose an iron disorder e.g. haemochromatosis, or a
CC genetic susceptibility to develop it.
XX
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCATGAGTGTCGCCGT 17
||||||||||||||||||
Db 1 ATCATGAGTGTCGCCGT 17

RESULT 2
AAC68462
ID AAC68462 standard; DNA; 32 BP.
XX
AC AAC68462;
XX
DT 21-FEB-2001 (first entry)
XX
DE Sequence surrounding HH mutation 24d7t.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ss.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Column 21; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 32 BP; 5 A; 5 C; 11 G; 11 T; 0 other;

Query Match 100.0%; Score 17; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCATGAGTGTCGCCGT 17
||||||||||||||||||
Db 10 ATCATGAGTGTCGCCGT 26

RESULT 3
ABL56391
ID ABL56391 standard; DNA; 30 BP.
XX
AC ABL56391;
XX
DT 22-JUL-2002 (first entry)
XX
DE Gene fragment which when mutated causes haemochromatosis.
XX
KW Mutation; solid phase amplification; haemochromatosis; cancer;
KW sickle-cell anaemia; beta-thalassemia; alpha-thalassemia; polymorphism;
KW cystic fibrosis; haemophilia; neurodegeneration; ss.
XX
OS Homo sapiens.
XX
PN WO200212557-A1.
XX
PD 14-FEB-2002.
XX
PF 08-AUG-2001; 2001WO-FR02574.
XX
PR 08-AUG-2000; 2000FR-0010425.
XX
PA (NUCL-) NUCLEICA.
XX
PI Cailloux F, Gobron S;
XX
DR WPI; 2002-269096/31.
XX
PT Detecting mutations in nucleic acid, useful e.g. for diagnosing
PT haemochromatosis, by solid phase amplification to incorporate
PT exonuclease resistant nucleotide -
XX
PS Example 2; Page 16; 43pp; French.
XX
CC The present sequence represents a fragment of the gene to which probe
CC ABL56390 hybridises. This probe was used to detect the mutation H63D,
CC which is responsible for haemochromatosis. The probe is used to
CC demonstrate the method of the invention. The specification describes
CC a method for detecting a mutation at position n in a target nucleic
CC acid by solid phase amplification process. The region of interest is
CC amplified on at least two separate supports (A, B) using at least one
CC primer linked, at its 5'-end, to the supports. The DNA strands are
CC then separated and strands in the suspension removed by washing.
CC Bound DNA sequences are hybridized to a probe, the 3'-end of which
CC hybridizes up to, at most, position n-1. The probe is elongated by
CC adding complementary nucleotides in the 5' to 3' direction, using a DNA
CC polymerase and a nucleotide derivative (dNTP*) that is resistant to
CC exonuclease. The dNTP* used is complementary to the mutation for support
CC A but to the wild type for support B. Products are digested with an
CC exonuclease so that only probes elongated by dNTP* are not degraded.
CC The supports are then washed and non-degraded probes detected
CC (in)directly. The method is used to detect mutations associated with
CC disease, especially haemochromatosis; sickle-cell anaemia; alpha or
CC beta-thalassemia; cystic fibrosis; haemophilia; neurodegeneration and
CC cancer. The method is also used to study polymorphisms of gene or an
CC entire genetic region and for detecting and/or identifying genetically
CC modified organisms.

```
XX
SQ   Sequence 30 BP; 6 A; 7 C; 10 G; 7 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 24;  Length 30;
  Best Local Similarity   94.1%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db          5 ATCATGAGAGTCGCCGT 21


RESULT 4
AAK98989
ID   AAK98989 standard; DNA; 31 BP.
XX
AC   AAK98989;
XX
DT   24-MAY-2002  (first entry)
XX
DE   Human probe target HHDT1 of haemochromatosis-associated mutation C187G.
XX
KW   Fluorescent detecting entity; melting curve analysis; genotyping;
KW   pathogen; probe; human; Factor V Leiden mutation; target; ss.
XX
OS   Homo sapiens.
XX
PN   WO200214555-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US25231.
XX
PR   11-AUG-2000; 2000US-224726P.
PR   16-OCT-2000; 2000US-240610P.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (IDAH-) IDAHO TECHNOLOGY INC.
XX
PI   Wittwer CT,  Crockett AO,  Caplin BE,  Stevenson W,  Wagner LA;
PI   Chen J,  Kusukawa N;
XX
DR   WPI; 2002-269208/31.
XX
PT   New probe useful for e.g. genotyping, comprises a single-labelled
PT   oligonucleotide having a sequence complementary to a locus of the
PT   target nucleic acid and a fluorescent label linked to an internal
PT   residue of the oligonucleotide  -
XX
PS   Example 1; Page 17; 73pp; English.
XX
CC   The invention relates to a new probe for analysing a target nucleic acid
CC   comprising of a fluorescent detecting entity consisting of a single-
CC   labelled oligonucleotide having a sequence complementary to a locus of
CC   the target nucleic acid and a fluorescent label linked to an internal
CC   residue of the oligonucleotide. The probe is useful in melting curve
CC   analysis, genotyping, detecting pathogens such as Salmonella, and in
CC   determining the presence of a target nucleic acid sequence in a
CC   biological sample. This polynucleotide sequence represents a probe target
CC   of the invention for melting analysis of haemochromatosis-associated
CC   mutation C187G.
XX
SQ   Sequence 31 BP; 6 A; 5 C; 10 G; 10 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 24;  Length 31;
  Best Local Similarity   94.1%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         10 ATCATGAGAGTCGCCGT 26


RESULT 5
AAC68461
ID   AAC68461 standard; DNA; 32 BP.
XX
AC   AAC68461;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Sequence surrounding HH mutation 24d7a.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Column 21; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 32 BP; 6 A; 5 C; 11 G; 10 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 22;  Length 32;
  Best Local Similarity   94.1%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         10 ATCATGAGAGTCGCCGT 26


RESULT 6
AAC68459
ID   AAC68459 standard; DNA; 40 BP.
XX
AC   AAC68459;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Sequence surrounding HH mutation 24d2 c.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
```

```
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Column 20; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 40 BP; 7 A; 7 C; 13 G; 13 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 22;  Length 40;
  Best Local Similarity   94.1%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||  ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 7
AAH78015
ID   AAH78015 standard; DNA; 47 BP.
XX
AC   AAH78015;
XX
DT   26-NOV-2001  (first entry)
XX
DE   DNA fragment with a mutation which is implicated in haemochromatosis.
XX
KW   DNA mutation; hereditary genetic disease; sickle cell anemia;
KW   thalassemia; cystic fibrosis; haemophilia; cancer; haemochromatosis; ds.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   mutation        22
FT                   /*tag=  a
FT                   /note= "this base is mutated to G"
XX
PN   WO200164945-A2.
XX
PD   07-SEP-2001.
XX
PF   01-MAR-2001; 2001WO-FR00604.
XX
PR   01-MAR-2000; 2000FR-0002614.
XX
PA   (NUCL-) NUCLEICA.
XX
PI   Cailloux F;
XX
DR   WPI; 2001-557783/62.
XX
PT   Detecting mutation in target nucleic acid, useful for detecting
PT   hereditary genetic diseases, comprises using chip whose electrical or
PT   optical property changes relative to the presence of hybridized probe -
XX
PS   Example 4; Page 17; 36pp; French.
XX
CC   The specification describes a method for detecting a mutation at
CC   a particular position in a target nucleic acid. The method comprises
CC   binding the target to a solid support, hybridizing a probe to the
CC   target, elongating the probe with nucleotide(s) resistant to
CC   exonuclease, digesting the probe with exonuclease and detecting bound
CC   nucleic acid. The mutation is in position 'n' in a target nucleic
CC   acid and the 3' extremity of the probe hybridises to position 'n'.
CC   The method is used to detect gene mutations implicated in disease,
CC   particularly hereditary genetic diseases, especially sickle cell
CC   anemia, alpha and beta thalassemias, cystic fibrosis, haemophilia
CC   and genes implicated in cancer. The present sequence represents a
CC   DNA fragment which comprises a mutation which is implicated in
CC   haemochromatosis. The mutation is detected using the method of the
CC   invention.
XX
SQ   Sequence 47 BP; 7 A; 12 C; 15 G; 13 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 22;  Length 47;
  Best Local Similarity   94.1%;  Pred. No. 53;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||  ||||||||
Db         20 ATCATGAGAGTCGCCGT 36


RESULT 8
AAF58246/c
ID   AAF58246 standard; DNA; 75 BP.
XX
AC   AAF58246;
XX
DT   24-APR-2001  (first entry)
XX
DE   Oligonucleotide D1121.
XX
KW   Electron-transfer group; ETM; mismatch; genotyping;
KW   gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO200107665-A2.
XX
PD   01-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US20476.
XX
PR   26-JUL-1999;   99US-0145695.
PR   17-MAR-2000; 2000US-0190259.
XX
PA   (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI   Umek RM;
XX
DR   WPI; 2001-159728/16.
XX
PT   Nucleic acids containing electron-transfer group, useful as labels in
PT   hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT   a single surface  -
XX
PS   Example 6; Page 127; 159pp; English.
XX
CC   The present invention relates to a composition comprising two nucleic
CC   acids each containing an electron-transfer group (ETM) having
CC   different redox potentials. The invention is used for electronic
CC   detection of nucleic acids, especially of substitutions (mismatches)
CC   and single-nucleotide polymorphisms, e.g. for genotyping,
```

```
CC   monitoring gene expression.
XX
SQ   Sequence 75 BP; 21 A; 24 C; 16 G; 14 T; 0 other;

  Query Match            90.6%;  Score 15.4;  DB 22;  Length 75;
  Best Local Similarity  94.1%;  Pred. No. 56;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| |||||||||
Db         32 ATCATGAGAGTCGCCGT 16


RESULT 9
AAF58231/c
ID   AAF58231 standard; DNA; 76 BP.
XX
AC   AAF58231;
XX
DT   24-APR-2001  (first entry)
XX
DE   Oligonucleotide D1121.
XX
KW   Electron-transfer group; ETM; mismatch; genotyping;
KW   gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO200107665-A2.
XX
PD   01-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US20476.
XX
PR   26-JUL-1999;   99US-0145695.
PR   17-MAR-2000; 2000US-0190259.
XX
PA   (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI   Umek RM;
XX
DR   WPI; 2001-159728/16.
XX
PT   Nucleic acids containing electron-transfer group, useful as labels in
PT   hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT   a single surface -
XX
PS   Example 2; Page 115; 159pp; English.
XX
CC   The present invention relates to a composition comprising two nucleic
CC   acids each containing an electron-transfer group (ETM) having
CC   different redox potentials. The invention is used for electronic
CC   detection of nucleic acids, especially of substitutions (mismatches)
CC   and single-nucleotide polymorphisms, e.g. for genotyping,
CC   monitoring gene expression.
XX
SQ   Sequence 76 BP; 21 A; 24 C; 17 G; 14 T; 0 other;

  Query Match            90.6%;  Score 15.4;  DB 22;  Length 76;
  Best Local Similarity  94.1%;  Pred. No. 56;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| |||||||||
Db         32 ATCATGAGAGTCGCCGT 16


RESULT 10
AAH02413
ID   AAH02413 standard; DNA; 100 BP.
XX
AC   AAH02413;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Human HLA-H exon 2 coding sequence fragment SEQ ID NO: 110.
XX
KW   Database; polymorphism; SNP; human; genetic marker; disease; infection;
KW   drug response; ds.
XX
OS   Homo sapiens.
XX
PN   WO200127857-A2.
XX
PD   19-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US28413.
XX
PR   13-OCT-1999;   99US-0159176.
PR   10-JUL-2000; 2000US-0217251.
PR   10-JUL-2000; 2000US-0217658.
PR   19-SEP-2000; 2000US-0663968.
XX
PA   (SEQU-) SEQUENOM INC.
XX
PI   Braun A, Koester H, Van Den Boom D, Ping Y, Rodi C, He L, Chiu N;
PI   Jurinke C;
XX
DR   WPI; 2001-273865/28.
XX
PT   Producing a database for identifying polymorphic genetic markers,
PT   comprises obtaining data relating to members of a healthy population
PT   and entering the information into a database -
XX
PS   Example 9; Page 303; 304pp; English.
XX
CC   The present invention provides a database of human samples obtained from
CC   healthy individuals which can be used to identify polymorphic genetic
CC   markers. Data obtained for the database can be used to sort the samples
CC   by parameters such as age, sex and ethnicity. This is useful in linking
CC   markers with diseases, susceptibility to infection and drug responses.
CC   The present sequence was used in an assay to demonstrate the uses of the
CC   database of the invention.
XX
SQ   Sequence 100 BP; 19 A; 22 C; 29 G; 30 T; 0 other;

  Query Match            90.6%;  Score 15.4;  DB 22;  Length 100;
  Best Local Similarity  94.1%;  Pred. No. 58;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| |||||||||
Db         46 ATCATGAGAGTCGCCGT 62


RESULT 11
AAI63897
ID   AAI63897 standard; cDNA; 596 BP.
XX
AC   AAI63897;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 105.
XX
KW   Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW   cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW   fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW   neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW   antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
KW   antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW   cardiovascular disorder; neurological disease; infection; human; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155308-A2.
```

XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01309.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX

DR WPI; 2001-488781/53.
DR P-PSDB; AAM43591.
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
PS Claim 1; SEQ ID NO 105; 664pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 596 BP; 133 A; 157 C; 175 G; 126 T; 5 other;

Query Match 90.6%; Score 15.4; DB 22; Length 596;
Best Local Similarity 94.1%; Pred. No. 72;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| |||||||||
Db        253 ATCATGAGAGTCGCCGT 269
```

RESULT 12
ABK49917
ID ABK49917 standard; cDNA; 1317 BP.
XX
AC ABK49917;
XX
DT 15-JUL-2002 (first entry)
XX
DE DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
XX
KW Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
KW iron absorption regulator; intracellular iron absorption; lung injury;
KW haemochromatosis; transfusion; thalassaemia; haemolytic anaemia;
KW chronic infection; transferrin receptor; TfR; brain tumour; cancer;
KW oxidative stress disorder; tissue damage; vascular disease;
KW inflammation; atherosclerosis; autoimmune disease;
KW inflammatory condition; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1317
FT /*tag= a
FT /product= "beta2M/HFE monochain"
XX
PN WO200224929-A2.
XX
PD 28-MAR-2002.
XX
PF 24-SEP-2001; 2001WO-US29873.
XX
PR 22-SEP-2000; 2000US-234843P.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (MCIN/) MCINNIS P.
XX
PI Ehrlich R, Rotem-Yehudar R, Laham N;
XX
DR WPI; 2002-383192/41.
DR P-PSDB; AAU80035.
XX
PT Soluble beta 2 microglobulin/HFE monochain useful for treating
PT iron-overload conditions e.g. thalassemia and chronic infections,
PT comprises human beta 2 microglobulin linked to alpha domains of HFE by
PT a linker peptide -
XX
PS Example 2; Fig 2; 77pp; English.
XX
CC The invention relates to a soluble polypeptide (I) of beta 2
CC microglobulin (beta2m)/HFE monochain comprising human beta2m (or its
CC analogue or active fragment), linked to alpha1-alpha3 domains of human
CC HFE (a central regulator of iron absorption; undefined), or its analogue
CC or active fragment, by a flexible linker peptide, or a functional
CC derivative or salt of (I). (I) is useful for reducing intracellular iron
CC absorption in patients having hereditary haemochromatosis, transfusions,
CC thalassaemias, haemolytic anaemia or chronic infections, and for
CC delivering a therapeutic to cells that over-express transferrin receptor
CC (TfR) which are preferably lymphocytes or leukocytes, across the blood-
CC brain barrier. (I) is further useful for treating brain tumour. (I)
CC is also useful for treating oxidative stress disorders resulting in
CC tissue damage e.g. vascular diseases, inflammation, atherosclerosis,
CC lung injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful
CC as a platform for drug delivery of therapeutic use for cancer,
CC autoimmune diseases and inflammatory conditions. The monochain manifests
CC specific characteristics advantageous for drug delivery systems. It is a
CC soluble, stable and fully conformed protein. It binds specifically to
CC transferrin receptor (TfR) and therefore targets cells that over-express
CC this receptor. It is continuously internalised by the target cells, thus
CC enabling efficient drug delivery. It dissociates from the receptor in the
CC cells, minimising side effects. It negatively regulates iron absorption,
CC reducing growth of undesired cells and preventing lymphocyte activation.
CC It is not diluted in the blood as is transferrin. It should not induce an
CC immune response since it is a self non-polymeric protein and delivery of
CC drugs via monochain is expected to overcome drug-resistance since it is a
CC natural TfR-binding protein. The present sequence represents the
CC coding sequence of beta2m/HFE monochain.
XX
SQ Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;

Query Match 90.6%; Score 15.4; DB 24; Length 1317;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| |||||||||
Db        521 ATCATGAGAGTCGCCGT 537
```

RESULT 13
AAT96691
ID AAT96691 standard; cDNA; 1440 BP.
XX
AC AAT96691;
XX
DT 14-APR-1998 (first entry)
XX
DE Hereditary haemochromatosis gene cDNA clone.
XX
KW Hereditary haemochromatosis; metal toxicity; diagnosis;
KW gene therapy; prenatal screening; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 222.1268
FT /*tag= a
FT mutation 408
FT /*tag= g

```
FT                      /note= "C to G substitution (24d2 mutation)
FT                             results in His to Asp substitution"
FT   variation          414
FT                      /*tag=  h
FT                      /note= "A to T substitution (24d7 variant)
FT                             results in Ser to Cys substitution"
FT   mutation           1066
FT                      /*tag=  i
FT                      /note= "G to A substitution (24d1 mutation
FT                             associated with HH), results in Cys to
FT                             Tyr substitution"
XX
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US06254.
XX
PR   23-MAY-1996;   96US-0652265.
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   P-PSDB; AAW36499.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis
PT   and treatment of hereditary haemochromatosis disease
XX
PS   Disclosure; Fig 4; 115pp; English.
XX
CC   This cDNA clone, designated cDNA24, is derived from human gene
CC   whose mutated form is associated with hereditary haemochromatosis
CC   (HH).  It was obtained from a directionally cloned plasmid-based
CC   cDNA library following identification of the HH locus in the HLA
CC   region of chromosome 6.  A single mutation (24d1) in the HH gene
CC   appears responsible for the majority of HH disease.  This comprises
CC   a G to A substitution that is present in 86% of affected
CC   chromosomes and in 4% of unaffected chromosomes.  It results in a
CC   Cys to Tyr substitution in the encoded protein (see AAW36499) at a
CC   critical disulphide bridge important for secondary structure.  The
CC   following are claimed: a 10825 bp genomic DNA sequence (I) (see
CC   AAT96690), the 1437 bp cDNA sequence (Ia) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a
CC   peptide product chosen from the HH gene product, its variants
CC   (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC   residues of these; an antibody produced using the peptide; a method
CC   to determine the presence or absence of the common HH gene
CC   mutation; an animal model for the HH disease; metal chelation
CC   agents, T-cell differentiation factors and therapeutic agents for
CC   the mitigation of injury due to oxidative process in vivo or
CC   mitigation of iron overload; a method for screening potential
CC   therapeutic agents for activity in connection with HH disease; an
CC   antisense oligonucleotide directed against a transcriptional
CC   product of a nucleic acid sequence as above; and oligonucleotides
CC   or pairs of oligonucleotides covering a range of nucleotides from
CC   (I), (Ia) or their variants, useful for detecting a polymorphism in
CC   the HH gene.  The invention also relates to methods for screening
CC   for HH homozygotes, to HH diagnosis, prenatal screening and
CC   diagnosis, and therapies of HH disease, including gene therapy,
CC   protein- and antibody-based therapeutics, and small molecule
CC   therapeutics.
XX
SQ   Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 18;  Length 1440;
  Best Local Similarity   94.1%;  Pred. No. 79;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||| |||||||
Db        406 ATCATGAGAGTCGCCGT 422


RESULT 14
AAC68429
ID   AAC68429 standard; DNA; 1440 BP.
XX
AC   AAC68429;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 4; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 22;  Length 1440;
  Best Local Similarity   94.1%;  Pred. No. 79;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||| |||||||
Db        406 ATCATGAGAGTCGCCGT 422


RESULT 15
AAC68430
ID   AAC68430 standard; DNA; 1440 BP.
XX
AC   AAC68430;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d1 mutation cDNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ss.
```

XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 4; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;

Query Match 90.6%; Score 15.4; DB 22; Length 1440;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| |||||||||
Db        406 ATCATGAGAGTCGCCGT 422
```

Search completed: September 12, 2003, 23:52:10
Job time : 14.0108 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 12, 2003, 23:31:00 ; Search time 103.933 Seconds
(without alignments)
3975.400 Million cell updates/sec

Title: US-09-981-606-30
Perfect score: 17
Sequence: 1 atcatgagtgtcgccgt 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		17	100.0	908	12	BI918632	BI918632 603176589
2	c	16	94.1	684	10	BG506985	BG506985 601861617
3		15.4	90.6	270	29	CC075265	CC075265 CSU-K33r.
4		15.4	90.6	325	13	BY352115	BY352115 BY352115
5		15.4	90.6	344	13	BY196171	BY196171 BY196171
6		15.4	90.6	346	13	BY210730	BY210730 BY210730
7		15.4	90.6	347	13	BY327323	BY327323 BY327323
8		15.4	90.6	351	13	BY319883	BY319883 BY319883
9		15.4	90.6	357	13	BY206107	BY206107 BY206107
10		15.4	90.6	359	13	BY170353	BY170353 BY170353
11		15.4	90.6	364	13	BY202250	BY202250 BY202250
12		15.4	90.6	366	13	BY168570	BY168570 BY168570
13		15.4	90.6	380	13	BY198206	BY198206 BY198206
14	c	15.4	90.6	384	10	BF883952	BF883952 PM4-ET020
15		15.4	90.6	388	13	BY313216	BY313216 BY313216
16		15.4	90.6	392	10	BF465475	BF465475 UI-M-CG0p
17		15.4	90.6	398	9	AA746759	AA746759 nx63f02.s
18		15.4	90.6	407	13	BY159932	BY159932 BY159932
19	c	15.4	90.6	464	9	AA217236	AA217236 mu89b05.r
20		15.4	90.6	481	10	BB851691	BB851691 BB851691
21		15.4	90.6	481	13	BQ561639	BQ561639 H4071E07-
22		15.4	90.6	482	10	BF249315	BF249315 NcEST3a09
23		15.4	90.6	489	10	BE994943	BE994943 UI-M-CG0p
24		15.4	90.6	502	10	BB858165	BB858165 BB858165
25	c	15.4	90.6	510	13	BQ305479	BQ305479 MR0-BT200
26		15.4	90.6	535	14	CB162561	CB162561 K-EST0223
27		15.4	90.6	542	14	CA569584	CA569584 K0445A07-
28		15.4	90.6	544	12	BM751283	BM751283 K-EST0027
29		15.4	90.6	560	9	AU279987	AU279987 AU279987
30		15.4	90.6	668	14	BY745026	BY745026 BY745026
31		15.4	90.6	714	14	BY747346	BY747346 BY747346
32	c	15.4	90.6	769	28	BZ085960	BZ085960 l1h38h05.
33		15.4	90.6	819	10	BG747345	BG747345 602704818
34		15.4	90.6	954	28	B12288	B12288 T2M2-Sp6 TA
35		15.4	90.6	1719	11	AK088986	AK088986 Mus muscu
36		15.4	90.6	1723	11	AK009581	AK009581 Mus muscu
37	c	15	88.2	930	10	BE617417	BE617417 601442056
38	c	15	88.2	948	10	BE901930	BE901930 601676872
39	c	15	88.2	988	10	BE616360	BE616360 601279161
40	c	14.4	84.7	175	14	CA998121	CA998121 S345A_F10
41	c	14.4	84.7	284	28	AY080089	AY080089 AY080089
42		14.4	84.7	297	10	BB605399	BB605399 BB605399
43	c	14.4	84.7	307	9	AV328885	AV328885 AV328885
44		14.4	84.7	315	9	AA787040	AA787040 k8c05a1.f
45		14.4	84.7	318	10	BG637391	BG637391 SD15386.5

ALIGNMENTS

RESULT 1
BI918632
LOCUS BI918632 908 bp mRNA linear EST 16-OCT-2001
DEFINITION 603176589F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240735 5', mRNA sequence.
ACCESSION BI918632
VERSION BI918632.1 GI:16182310
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11607 row: a column: 24
High quality sequence start: 3

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            High quality sequence stop: 708.
FEATURES             Location/Qualifiers
     source          1. .908
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240735"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      191 a    276 c    232 g    209 t
ORIGIN

  Query Match             100.0%;  Score 17;  DB 12;  Length 908;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db        553 ATCATGAGTGTCGCCGT 569


RESULT 2
BG506985/c
LOCUS       BG506985                684 bp    mRNA    linear   EST 27-MAR-2001
DEFINITION  601861617F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4071077 5',
            mRNA sequence.
ACCESSION   BG506985
VERSION     BG506985.1  GI:13468502
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM916  row: b  column: 06
            High quality sequence stop: 469.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4071077"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
BASE COUNT      250 a    142 c    127 g    165 t
ORIGIN

  Query Match             94.1%;  Score 16;  DB 10;  Length 684;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCATGAGTGTCGCCGT 17
              ||||||||||||||||
Db        631 TCATGAGTGTCGCCGT 616


RESULT 3
CC075265
LOCUS       CC075265                270 bp    DNA     linear   GSS 16-APR-2003
DEFINITION  CSU-K33r.7G6.SP6 CSU-K33r Aedes aegypti genomic clone CSU-K33r.7G6,
            genomic survey sequence.
ACCESSION   CC075265
VERSION     CC075265.1  GI:29916787
KEYWORDS    GSS.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
REFERENCE   1  (bases 1 to 270)
  AUTHORS   Loftus,B., Shetty,J., Severson,D., Brown,S. and Knudson,D.
  TITLE     End sequencing of Aedes aegypti BACs
  JOURNAL   Unpublished
COMMENT     Other_GSSs: CSU-K33r.7G6.T7
            Contact: Brendan Loftus
            Department of Eukaryotic Genomics
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: enta@tigr.org
            Library was provided by Susan Brown and Dennis Knudson at Colorado
            State University.
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .270
                     /organism="Aedes aegypti"
                     /mol_type="genomic DNA"
                     /strain="Rexville"
                     /db_xref="taxon:7159"
                     /clone="CSU-K33r.7G6"
                     /clone_lib="CSU-K33r"
                     /note="Vector: pBeloBAC11; Site_1: HindIII"
BASE COUNT       96 a     47 c     65 g     62 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 29;  Length 270;
  Best Local Similarity   94.1%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||| ||||||||||
Db        153 ATCATCAGTGTCGCCGT 169


RESULT 4
BY352115
LOCUS       BY352115                325 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  BY352115 RIKEN full-length enriched, whole joints Mus musculus cDNA
            clone L830026O07 5', mRNA sequence.
ACCESSION   BY352115
VERSION     BY352115.1  GI:26581603
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
```

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 325)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .325
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L830026007"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
BASE COUNT 55 a 97 c 96 g 77 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 13; Length 325;
Best Local Similarity 94.1%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATCATGAGTGTCGCCGT 17
||||||| |||||||
Db 293 ATCATGAGAGTCGCCGT 309

RESULT 5
BY196171
LOCUS BY196171 344 bp mRNA linear EST 10-DEC-2002
DEFINITION BY196171 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730024B08 5', mRNA sequence.
ACCESSION BY196171
VERSION BY196171.1 GI:26375480
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 344)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane

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            ,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.
            , Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.
            , Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
            ,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
            Submission
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             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
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            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .344
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                     /db_xref="taxon:10090"
                     /clone="F730024B08"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
BASE COUNT       70 a     89 c    103 g     82 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 13;  Length 344;
  Best Local Similarity   94.1%;  Pred. No. 7.2e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
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Db        282 ATCATGAGAGTCGCCGT 298


RESULT 6
BY210730
LOCUS       BY210730                346 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY210730 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730317N09 5', mRNA sequence.
ACCESSION   BY210730
VERSION     BY210730.1  GI:26391303
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.
            , Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
            Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
            Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
            Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
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            ,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.
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            King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
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            ,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
            Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
            Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring
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            ,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale
            ,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y.,
            Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa
            ,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
            Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura
            ,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.
            , Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii
            ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
            ,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
            ,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
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            ,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.
            , Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.
            , Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
            ,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
            Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="F730317N09"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
BASE COUNT       60 a    101 c    102 g     82 t      1 others
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 13;  Length 346;
  Best Local Similarity   94.1%;  Pred. No. 7.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 ATCATGAGTGTCGCCGT 17
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Db        293 ATCATGAGAGTCGCCGT 309


RESULT 7
BY327323
LOCUS       BY327323                347 bp    mRNA    linear   EST 11-DEC-2002
DEFINITION  BY327323 RIKEN full-length enriched, synovial fibroblasts Mus
            musculus cDNA clone L030041G21 5', mRNA sequence.
ACCESSION   BY327323
VERSION     BY327323.1  GI:26517890
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 347)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.
            , Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
            Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
            Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
            Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
            ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
            ,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.
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            ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
            ,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
            ,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
            ,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.
            , Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.
            , Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
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            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
            Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
            Fleming street 16672 Vari,Greece ) whose assistance we gratefully
            acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1..347
                     /organism="Mus musculus"
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                     /clone_lib="RIKEN full-length enriched, synovial
                     fibroblasts"
BASE COUNT       60 a    103 c    102 g     82 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 13;  Length 347;
  Best Local Similarity   94.1%;  Pred. No. 7.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
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Db        293 ATCATGAGAGTCGCCGT 309


RESULT 8
BY319883
LOCUS       BY319883                351 bp    mRNA    linear   EST 11-DEC-2002
DEFINITION  BY319883 RIKEN full-length enriched, osteoclast-like cell Mus
            musculus cDNA clone I420103B14 5', mRNA sequence.
ACCESSION   BY319883
VERSION     BY319883.1  GI:26510220
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.
            , Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
            Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
            Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
            Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
            ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
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            King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
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            Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring
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            ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
            ,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
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TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
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COMMENT Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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Tissues were provided by Takashi Ishikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura,Kanazawa-ku,Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .351
/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="I420103B14"
/cell_type="osteoclast-like cell"
/clone_lib="RIKEN full-length enriched, osteoclast-like cell"
BASE COUNT 60 a 104 c 103 g 84 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 13; Length 351;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATCATGAGTGTCGCCGT 17
||||||||| |||||||||
Db 273 ATCATGAGAGTCGCCGT 289

RESULT 9
BY206107
LOCUS BY206107 357 bp mRNA linear EST 10-DEC-2002
DEFINITION BY206107 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730222A16 5', mRNA sequence.
ACCESSION BY206107
VERSION BY206107.1 GI:26385983
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 357)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers

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                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
BASE COUNT       63 a    106 c    104 g     84 t
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 13;  Length 357;
  Best Local Similarity   94.1%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db        293 ATCATGAGAGTCGCCGT 309


RESULT 10
BY170353
LOCUS       BY170353                359 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY170353 RIKEN full-length enriched, bone marrow macrophage Mus
            musculus cDNA clone I830082A04 5', mRNA sequence.
ACCESSION   BY170353
VERSION     BY170353.1  GI:26306999
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.
            , Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
            Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
            Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
            Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
            ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
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            Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
            Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring
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            ,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale
            ,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y.,
            Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa
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            Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura
            ,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.
            , Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii
            ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
            ,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
            ,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
            ,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.
            , Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.
            , Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
            ,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
            Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by David A. Hume ( Depts. of Biochemistry
            and Microbiology/Parasitology Institute for Molecular Bioscience
            University of Queensland Brisbane,Q 4072 Australia ) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .359
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
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                      /tissue_type="bone marrow"
                      /cell_type="macrophage"
                      /clone_lib="RIKEN full-length enriched, bone marrow
                      macrophage"
BASE COUNT       60 a    101 c    107 g     90 t      1 others
ORIGIN

  Query Match             90.6%;  Score 15.4;  DB 13;  Length 359;
  Best Local Similarity   94.1%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db        312 ATCATGAGAGTCGCCGT 328


RESULT 11
BY202250
LOCUS       BY202250                364 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY202250 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730112A15 5', mRNA sequence.
ACCESSION   BY202250
VERSION     BY202250.1  GI:26381880
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 364)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.
            , Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
            Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
            Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
            Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
            ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
            ,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.
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, Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons ,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki ,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring ,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou ,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale ,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa ,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura ,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K. , Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata ,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander ,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane ,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A. , Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K. , Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami ,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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FEATURES Location/Qualifiers
source 1. .364
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F730112A15"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells"

BASE COUNT 65 a 107 c 105 g 87 t

ORIGIN

Query Match 90.6%; Score 15.4; DB 13; Length 364;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db        286 ATCATGAGAGTCGCCGT 302
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RESULT 12
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LOCUS BY168570 366 bp mRNA linear EST 10-DEC-2002
DEFINITION BY168570 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830072F07 5', mRNA sequence.
ACCESSION BY168570
VERSION BY168570.1 GI:26305216
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 366)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H. , Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest ,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A. , Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons ,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki ,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring ,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou ,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale ,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa ,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura ,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K. , Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata ,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander ,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

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FEATURES             Location/Qualifiers
     source          1. .366
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                     /tissue_type="bone marrow"
                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched, bone marrow
                     macrophage"
BASE COUNT       63 a    103 c    108 g     92 t
ORIGIN
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Query Match 90.6%; Score 15.4; DB 13; Length 366;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATCATGAGTGTCGCCGT 17
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Db        313 ATCATGAGAGTCGCCGT 329
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RESULT 13
BY198206

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LOCUS       BY198206                380 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY198206 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
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ACCESSION   BY198206
VERSION     BY198206.1  GI:26377594
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 380)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.
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            Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
            ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
            ,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.
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            Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
            King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
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            , Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii
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            ,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
            ,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.
            , Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.
            , Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
            ,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
            Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 384)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM4&t2=PM4-ET0209-151200-003-f07&t3=2000-12-15&t4=1)
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High quality sequence start: 17
High quality sequence stop: 384.
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BASE COUNT 92 a 112 c 87 g 93 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 10; Length 384;
Best Local Similarity 94.1%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION BY313216 RIKEN full-length enriched, osteoclast-like cell Mus musculus cDNA clone I420003G14 5', mRNA sequence.
ACCESSION BY313216
VERSION BY313216.1 GI:26503553
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 388)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Takashi Ishikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura,Kanazawa-ku,Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
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  Best Local Similarity   94.1%;  Pred. No. 7.6e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Scoring table: IDENTITY_NUC
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	17	100.0	32	3	US-08-834-497A-44	Sequence 44, Appl
	5	17	100.0	32	3	US-09-503-444A-44	Sequence 44, Appl
	6	15.4	90.6	32	3	US-08-652-265-43	Sequence 43, Appl
	7	15.4	90.6	32	3	US-08-834-497A-43	Sequence 43, Appl
	8	15.4	90.6	32	3	US-09-503-444A-43	Sequence 43, Appl
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	45	13.8	81.2	1440	3	US-08-652-265-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-277-457-30
; Sequence 30, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Barry E.
; APPLICANT: Sawada-Hirai, Ritsuko
; APPLICANT: Barton, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERENCE: 10653/002001
; CURRENT APPLICATION NUMBER: US/09/277,457
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: S65C Mutation
US-09-277-457-30

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; Patent No. 6509442
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Barry E.
; APPLICANT: Sawada-Hirai, Ritsuko
; APPLICANT: Barton, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERENCE: 24065-004 DIV
; CURRENT APPLICATION NUMBER: US/09/679,729
; CURRENT FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
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; LENGTH: 17
; TYPE: DNA

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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: S65C Mutation
US-09-679-729-30

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Db          1 ATCATGAGTGTCGCCGT 17


RESULT 3
US-08-652-265-44
; Sequence 44, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-652-265-44

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; Sequence 44, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-834-497A-44

  Query Match             100.0%;  Score 17;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.82;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db         10 ATCATGAGTGTCGCCGT 26


RESULT 5
US-09-503-444A-44
; Sequence 44, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
```

```
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-503-444A-44

  Query Match             100.0%;  Score 17;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.82;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db         10 ATCATGAGTGTCGCCGT 26


RESULT 6
US-08-652-265-43
; Sequence 43, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-652-265-43

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 32;
  Best Local Similarity   94.1%;  Pred. No. 6.8;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||| ||||||||
Db         10 ATCATGAGAGTCGCCGT 26


RESULT 7
US-08-834-497A-43
; Sequence 43, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
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```
;       APPLICATION NUMBER:  US 08/632,673
;       FILING DATE:  16-APR-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/630,912
;       FILING DATE:  04-APR-1996
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M.
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  8907-0056-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-493-4935
;       TELEFAX:  650-493-5556
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  32 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-834-497A-43

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 32;
  Best Local Similarity   94.1%;  Pred. No. 6.8;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||| |||||||
Db         10 ATCATGAGAGTCGCCGT 26


RESULT 8
US-09-503-444A-43
; Sequence 43, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-503-444A-43

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 32;
  Best Local Similarity   94.1%;  Pred. No. 6.8;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||| |||||||
Db         10 ATCATGAGAGTCGCCGT 26


RESULT 9
US-08-652-265-41
; Sequence 41, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-652-265-41

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 40;
  Best Local Similarity   94.1%;  Pred. No. 7;
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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 10
US-08-834-497A-41
; Sequence 41, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-834-497A-41

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 40;
  Best Local Similarity   94.1%;  Pred. No. 7;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 11
US-09-503-444A-41
; Sequence 41, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-503-444A-41

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 40;
  Best Local Similarity   94.1%;  Pred. No. 7;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 12
US-09-252-991A-9808/c
; Sequence 9808, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
```

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;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 9808
;   LENGTH: 687
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9808

  Query Match             90.6%;  Score 15.4;  DB 4;  Length 687;
  Best Local Similarity   94.1%;  Pred. No. 10;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
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RESULT 13
US-08-652-265-9
; Sequence 9, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(414, "a")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d7
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "g")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-08-652-265-9

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 1440;
  Best Local Similarity   94.1%;  Pred. No. 12;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||| ||||||||
Db        406 ATCATGAGAGTCGCCGT 422


RESULT 14
US-08-652-265-10
; Sequence 10, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MCLECULE TYPE:  cDNA
;    FEATURE:
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;       NAME/KEY:  CDS
;       LOCATION:  222..1268
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(1066, "a")
;       OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d1
US-08-652-265-10

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 1440;
  Best Local Similarity   94.1%;  Pred. No. 12;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| |||||||||
Db        406 ATCATGAGAGTCGCCGT 422


RESULT 15
US-08-834-497A-9
; Sequence 9, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1440 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  222..1268
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(408, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(414, "a")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d7
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(1066, "g")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-9

  Query Match             90.6%;  Score 15.4;  DB 3;  Length 1440;
  Best Local Similarity   94.1%;  Pred. No. 12;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| |||||||||
Db        406 ATCATGAGAGTCGCCGT 422


Search completed: September 13, 2003, 01:51:07
Job time : 4.06859 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 12, 2003, 23:45:10 ; Search time 10.6787 Seconds
(without alignments)
3864.876 Million cell updates/sec

Title: US-09-981-606-30
Perfect score: 17
Sequence: 1 atcatgagtgtcgccgt 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		17	100.0	17	12	US-09-981-606-30	Sequence 30, Appl
2		17	100.0	21	12	US-10-142-729-68	Sequence 68, Appl
3		17	100.0	32	12	US-10-138-888-44	Sequence 44, Appl
4	c	17	100.0	39	12	US-10-142-729-62	Sequence 62, Appl
5		17	100.0	1440	12	US-10-138-888-77	Sequence 77, Appl
6		17	100.0	10825	12	US-10-138-888-79	GENERAL INFORMA
7		15.4	90.6	21	12	US-10-142-729-67	Sequence 67, Appl
8		15.4	90.6	31	11	US-09-927-842-43	Sequence 43, Appl
9		15.4	90.6	32	12	US-10-138-888-43	Sequence 43, Appl
10	c	15.4	90.6	39	12	US-10-142-729-61	Sequence 61, Appl
11		15.4	90.6	40	12	US-10-138-888-41	Sequence 41, Appl
12	c	15.4	90.6	40	12	US-10-142-729-63	Sequence 63, Appl
13		15.4	90.6	46	11	US-09-940-244-206	Sequence 206, App
14		15.4	90.6	46	12	US-10-290-386-206	Sequence 206, App
15		15.4	90.6	1440	12	US-10-138-888-9	Sequence 9, Appli
16		15.4	90.6	1440	12	US-10-138-888-10	Sequence 10, Appl
17		15.4	90.6	2506	12	US-09-981-606-1	Sequence 1, Appli
18		15.4	90.6	5982	13	US-10-016-634A-25	Sequence 25, Appl
19		15.4	90.6	10825	12	US-10-138-888-1	GENERAL INFORMA
20		15.4	90.6	10825	12	US-10-138-888-3	GENERAL INFORMA
21		15.4	90.6	12146	12	US-09-981-606-27	Sequence 27, Appl
22	c	15.4	90.6	235033	14	US-10-301-844-1	Sequence 1, Appli
23	c	15.4	90.6	237326	14	US-10-301-844-2	Sequence 2, Appli
24	c	14.4	84.7	1791	10	US-09-974-300-1076	Sequence 1076, Ap
25	c	14	82.4	65	12	US-09-908-975-2356	Sequence 2356, Ap
26	c	14	82.4	375	10	US-09-974-300-7046	Sequence 7046, Ap
27	c	14	82.4	9025608	14	US-10-156-761-1	Sequence 1, Appli
28	c	13.8	81.2	27	11	US-09-927-842-41	Sequence 41, Appl
29	c	13.8	81.2	27	11	US-09-927-842-42	Sequence 42, Appl
30	c	13.8	81.2	28	11	US-09-927-842-40	Sequence 40, Appl
31		13.8	81.2	31	11	US-09-927-842-44	Sequence 44, Appl
32		13.8	81.2	40	12	US-10-138-888-42	Sequence 42, Appl
33	c	13.8	81.2	40	12	US-10-142-729-64	Sequence 64, Appl
34		13.8	81.2	46	11	US-09-940-244-207	Sequence 207, App
35		13.8	81.2	46	12	US-10-290-386-207	Sequence 207, App
36	c	13.8	81.2	205	9	US-09-815-242-2087	Sequence 2087, Ap
37	c	13.8	81.2	382	10	US-09-983-965-5783	Sequence 5783, Ap
38	c	13.8	81.2	445	10	US-09-880-107-1944	Sequence 1944, Ap
39		13.8	81.2	680	11	US-09-983-802-144	Sequence 144, App
40		13.8	81.2	756	12	US-10-238-075-337	Sequence 337, App
41		13.8	81.2	1113	14	US-10-156-761-3094	Sequence 3094, Ap
42		13.8	81.2	1166	10	US-09-860-670-231	Sequence 231, App
43		13.8	81.2	1266	13	US-10-027-632-124762	Sequence 124762,
44		13.8	81.2	1278	10	US-09-738-626-3444	Sequence 3444, Ap
45		13.8	81.2	1326	14	US-10-021-723A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-981-606-30
; Sequence 30, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg et al.
; TITLE OF INVENTION: Mutations associated with iron disorders
; FILE REFERENCE: 24065-004CON
; CURRENT APPLICATION NUMBER: US/09/981,606
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
; OTHER INFORMATION: primer
US-09-981-606-30

Query Match 100.0%; Score 17; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db          1 ATCATGAGTGTCGCCGT 17
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RESULT 2
US-10-142-729-68
; Sequence 68, Application US/10142729
; Publication No. US20030165888A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.

```
;  TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
;  TITLE OF INVENTION:  COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
;  FILE REFERENCE: OASBIO.005A
;  CURRENT APPLICATION NUMBER: US/10/142,729
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 60/306,229
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: 09/136,080
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/060,673
;  PRIOR FILING DATE: 1997-10-02
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 2
;   OTHER INFORMATION: n = modified base
US-10-142-729-68

  Query Match             100.0%;  Score 17;  DB 12;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.9;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
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Db          4 ATCATGAGTGTCGCCGT 20


RESULT 3
US-10-138-888-44
; Sequence 44, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 44:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-138-888-44

  Query Match             100.0%;  Score 17;  DB 12;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db         10 ATCATGAGTGTCGCCGT 26


RESULT 4
US-10-142-729-62/c
; Sequence 62, Application US/10142729
; Publication No. US20030165888A1
; GENERAL INFORMATION:
;  APPLICANT: Brown, Bob D.
;  APPLICANT:  Riley, Timothy A.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
;  TITLE OF INVENTION:  COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
;  FILE REFERENCE: OASBIO.005A
;  CURRENT APPLICATION NUMBER: US/10/142,729
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 60/306,229
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: 09/136,080
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/060,673
;  PRIOR FILING DATE: 1997-10-02
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1
;   OTHER INFORMATION: n = modified base
US-10-142-729-62

  Query Match             100.0%;  Score 17;  DB 12;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 5.2;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db         31 ATCATGAGTGTCGCCGT 15


RESULT 5
US-10-138-888-77
; Sequence 77, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
```

```
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 77:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1440 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  222..1268
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(414, "t")
;            OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;            (HH)"
;            /label= 24d7
;       SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-138-888-77

  Query Match             100.0%;  Score 17;  DB 12;  Length 1440;
  Best Local Similarity   100.0%;  Pred. No. 6.8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              |||||||||||||||||
Db        406 ATCATGAGTGTCGCCGT 422


RESULT 6
US-10-138-888-79
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;            OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;            (HH) protein containing the 24d7 mutation"
;            /note= "Hereditary Hemochromatosis
;            (HH)gene 24d7 allele"
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  140..7319
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  5507..6023
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(3878, "t")
;            OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;            (HH)"
;            /label= 24d7
;       SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-138-888-79

  Query Match             100.0%;  Score 17;  DB 12;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
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Db       3870 ATCATGAGTGTCGCCGT 3886


RESULT 7
US-10-142-729-67
; Sequence 67, Application US/10142729
; Publication No. US20030165888A1
; GENERAL INFORMATION:
;  APPLICANT: Brown, Bob D.
```

```
;  APPLICANT:  Riley, Timothy A.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
;  TITLE OF INVENTION:  COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
;  FILE REFERENCE: OASBIO.005A
;  CURRENT APPLICATION NUMBER: US/10/142,729
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 60/306,229
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: 09/136,080
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/060,673
;  PRIOR FILING DATE: 1997-10-02
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 2
;   OTHER INFORMATION: n = modified base
US-10-142-729-67

  Query Match             90.6%;  Score 15.4;  DB 12;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 40;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||  ||||||||
Db          4 ATCATGAGAGTCGCCGT 20


RESULT 8
US-09-927-842-43
; Sequence 43, Application US/09927842
; Publication No. US20030022177A1
; GENERAL INFORMATION:
;  APPLICANT: Wittwer, Carl
;  APPLICANT:  Crockett, Andrew
;  APPLICANT:  Caplin, Brian
;  APPLICANT:  Stevenson, Wade
;  APPLICANT:  Wagner, Lori
;  APPLICANT:  Chen, Jian
;  APPLICANT:  Kusukawa, No. US20030022177Aliko
;  TITLE OF INVENTION: Single-Labeled Oligonucleotide Probes for Homogeneous Nucleic Aci
;  TITLE OF INVENTION:  Sequence Analysis
;  FILE REFERENCE: 7475-67328
;  CURRENT APPLICATION NUMBER: US/09/927,842
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: US 60/224,726
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: US 60/240,610
;  PRIOR FILING DATE: 2000-10-16
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-927-842-43

  Query Match             90.6%;  Score 15.4;  DB 11;  Length 31;
  Best Local Similarity   94.1%;  Pred. No. 41;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||  ||||||||
Db         10 ATCATGAGAGTCGCCGT 26


RESULT 9
US-10-138-888-43
; Sequence 43, Application US/10138888
; Publication No. US20030148972A1
;  GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;  INFORMATION FOR SEQ ID NO: 43:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-138-888-43

  Query Match             90.6%;  Score 15.4;  DB 12;  Length 32;
  Best Local Similarity   94.1%;  Pred. No. 41;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||  ||||||||
Db         10 ATCATGAGAGTCGCCGT 26


RESULT 10
US-10-142-729-61/c
; Sequence 61, Application US/10142729
; Publication No. US20030165888A1
; GENERAL INFORMATION:
;  APPLICANT: Brown, Bob D.
;  APPLICANT:  Riley, Timothy A.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
```

```
;  TITLE OF INVENTION:  COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
;  FILE REFERENCE: OASBIO.005A
;  CURRENT APPLICATION NUMBER: US/10/142,729
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 60/306,229
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: 09/136,080
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/060,673
;  PRIOR FILING DATE: 1997-10-02
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1
;   OTHER INFORMATION: n = modified base
US-10-142-729-61

  Query Match             90.6%;  Score 15.4;  DB 12;  Length 39;
  Best Local Similarity   94.1%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         31 ATCATGAGAGTCGCCGT 15


RESULT 11
US-10-138-888-41
; Sequence 41, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;        APPLICANT: Thomas, Winston J.
;                   Drayna, Dennis T.
;                   Feder, John N.
;                   Gnirke, Andreas
;                   Ruddy, David
;                   Tsuchihashi, Zenta
;                   Wolff, Roger K.
;        TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;        NUMBER OF SEQUENCES: 79
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/138,888
;             FILING DATE: 02-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/632,673
;             FILING DATE: 16-APR-1996
;             APPLICATION NUMBER: US 08/630,912
;             FILING DATE: 04-APR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brian M. Poissant
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-095-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 41:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 40 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-138-888-41

  Query Match             90.6%;  Score 15.4;  DB 12;  Length 40;
  Best Local Similarity   94.1%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 12
US-10-142-729-63/c
; Sequence 63, Application US/10142729
; Publication No. US20030165888A1
; GENERAL INFORMATION:
;  APPLICANT: Brown, Bob D.
;  APPLICANT:  Riley, Timothy A.
;  TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
;  TITLE OF INVENTION:  COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
;  FILE REFERENCE: OASBIO.005A
;  CURRENT APPLICATION NUMBER: US/10/142,729
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 60/306,229
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: 09/136,080
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/060,673
;  PRIOR FILING DATE: 1997-10-02
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Oligonucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1
;   OTHER INFORMATION: n = modified base
US-10-142-729-63

  Query Match             90.6%;  Score 15.4;  DB 12;  Length 40;
  Best Local Similarity   94.1%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         25 ATCATGAGAGTCGCCGT 9


RESULT 13
US-09-940-244-206
; Sequence 206, Application US/09940244
; Publication No. US20030044796A1
; GENERAL INFORMATION:
;  APPLICANT: Neri, Bruce P.
;  APPLICANT:  Hall, Jeff G.
```

```
;  APPLICANT:  Lyamichev, Victor
;  APPLICANT:  Smith, Lloyd M.
;  TITLE OF INVENTION: Reactions on Dendrimers
;  FILE REFERENCE: FORS-06478
;  CURRENT APPLICATION NUMBER: US/09/940,244
;  CURRENT FILING DATE:  2002-05-06
;  NUMBER OF SEQ ID NOS: 422
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 206
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-940-244-206

  Query Match             90.6%;  Score 15.4;  DB 11;  Length 46;
  Best Local Similarity   94.1%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 14
US-10-290-386-206
; Sequence 206, Application US/10290386
; Publication No. US20030152971A1
; GENERAL INFORMATION:
;  APPLICANT: Lyamichev, Victor
;  APPLICANT:  Neri, Bruce P.
;  APPLICANT:  Hall, Jeff G.
;  APPLICANT:  Lukowiak, Andrew A.
;  TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences
;  FILE REFERENCE: FORS-07459
;  CURRENT APPLICATION NUMBER: US/10/290,386
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: 60/361,060
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/344,946
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: 09/713,601
;  PRIOR FILING DATE: 2000-11-15
;  PRIOR APPLICATION NUMBER: 09/381,212
;  PRIOR FILING DATE: 2000-02-08
;  PRIOR APPLICATION NUMBER: 09/350,309
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 08/823,516
;  PRIOR FILING DATE: 1997-03-24
;  PRIOR APPLICATION NUMBER: 08/759,038
;  PRIOR FILING DATE: 1996-12-02
;  PRIOR APPLICATION NUMBER: 08/756,386
;  PRIOR FILING DATE: 1996-11-26
;  PRIOR APPLICATION NUMBER: 08/682,853
;  PRIOR FILING DATE: 1996-07-12
;  PRIOR APPLICATION NUMBER: 08/599,491
;  PRIOR FILING DATE: 1996-01-24
;  NUMBER OF SEQ ID NOS: 253
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 206
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-290-386-206

  Query Match             90.6%;  Score 15.4;  DB 12;  Length 46;
  Best Local Similarity   94.1%;  Pred. No. 42;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||| ||||||||
Db         19 ATCATGAGAGTCGCCGT 35


RESULT 15
US-10-138-888-9
; Sequence 9, Application US/10138888
; Publication No. US20030148972A1
;  GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;  INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1440 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  222..1268
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(408, "c")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d2
;       FEATURE:
;            NAME/KEY:  allele
;            LOCATION:  replace(414, "a")
;            OTHER INFORMATION:  /phenotype= "normal or wild-type
;            (unaffected)"
;            /label= 24d7
;       FEATURE:
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;             NAME/KEY:  allele
;             LOCATION:  replace(1066, "g")
;             OTHER INFORMATION:  /phenotype= "normal or wild-type
;             (unaffected)"
;             /label= 24dl
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-138-888-9

  Query Match             90.6%;  Score 15.4;  DB 12;  Length 1440;
  Best Local Similarity   94.1%;  Pred. No. 54;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATCATGAGTGTCGCCGT 17
              ||||||||  ||||||||
Db        406 ATCATGAGAGTCGCCGT 422


Search completed: September 13, 2003, 01:57:07
Job time : 15.6787 secs
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; Sequence 1, Application US/09981606
; GENERAL INFORMATION:
; APPLICANT: Rothenberg et al.
; TITLE OF INVENTION: Mutations associated with iron disorders
; FILE REFERENCE: 24065-004CON
; CURRENT APPLICATION NUMBER: US/09/981,606
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Homo sapiens
09981606-1A

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tgctgcgttcacactctctgcactacctcttcatgggtgcctcagagcaggaccttggtctttccttgtt
tgaagctttgggctacgtggatgaccagctgttcgtgttctatgatcatgagtgtcgccgtgtggagccc
cgaactccatgggtttccagtagaatttcaagccagatgtggctgcagctgagtcagagtctgaaagggt
gggatcacatgttcactgttgacttctggactattatggaaaatcacaaccacagcaaggagtcccacac
cctgcaggtcatcctgggctgtgaaatgcaagaagacaacagtaccgagggctactggaagtacgggtat
gatgggcaggaccaccttgaattctgccctgacacactggattggagagcagcagaacccagggcctggc
ccaccaagctggagtgggaaaggcacaagattcgggccaggcagaacagggcctacctggagagggactg
ccctgcacagctgcagcagttgctggagctggggagaggtgttttggaccaacaagtgcctcctttggtg
aaggtgacacatcatgtgacctcttcagtgaccactctacggtgtcgggccttgaactactacccccaga
acatcaccatgaagtggctgaaggataagcagccaatggatgccaaggagttcgaacctaaagacgtatt
gcccaatggggatgggacctaccagggctggataaccttggctgtacccccttggggaagagcagagatat
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tgacctctcccctggaactgtctctcatgaacctcaagctgcatctagaggcttccttcatttcctccgt
cacctcagagacatacacctatgtcatttcatttcctatttttggaagaggactccttaaatttggggga
cttacatgattcatttaacatctgagaaaagctttgaaccctgggacgtggctagtcataaccttacca
gatttttacacatgtatctatgcatttttctggacccgttcaacttttccttttgaatcctctctctgtgtt
acccagtaactcatctgtcaccaagccttggggattcttccatctgattgtgatgtgagttgcacagcta
tgaaggctgtgcactgcacgaatggaagaggcacctgtcccagaaaaagcatcatggctatctgtgggta
gtatgatgggtgtttttagcaggtaggaggcaaatatcttgaaaggggttgtgaagaggtgtttttttcta
attggcatgaaggtgtcatacagatttgcaaagtttaatggtgccttcatttgggatgctactctagtat
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ggatgataaaagcacttacttcgtgtccgactctttctgagcacctacttacatgcattactgcatgcact
tcttacaataatttctatgagataggtactattatccccatttctttttttaaatgaagaaagtgaagtagg
ccgggcacggtggctcgcgcctgtggtcccagggtgctgagattgcaggtgtgagccaccctgcccagcc
gtcaaaagagtcttaatatatatatccagatggcatgtgtttacttttatgttactacatgcacttggctg
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ttagaaaagttatgtagaaaaaagtaaatgtgatttacgctcattgtagaaaagctataaaatgaataca
attaaagctgttatttaattagccagtgaaaaactattaacaacttgtctattacctgttagtattattg
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; Sequence 1, Application US/09981606
; GENERAL INFORMATION:
; APPLICANT: Rothenberg et al.
; TITLE OF INVENTION: Mutations associated with iron disorders
; FILE REFERENCE: 24065-004CON
; CURRENT APPLICATION NUMBER: US/09/981,606
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Homo sapiens
09981606-1B

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gggatcacatgttcactgttgacttctggactattatggaaaatcacaaccacagcaaggagtcccacac
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aaggtgacacatcatgtgacctcttcagtgaccactctacggtgtcgggccttgaactactacccccaga
acatcaccatgaagtggctgaaggataagcagccaatggatgccaaggagttcgaacctaaagacgtatt
gcccaatggggatgggacctaccagggctggataaccttggctgtacccccttggggaagagcagagatat
acgtnccaggtggagcacccaggcctggatcagcccctcattgtgatctgggagccctcaccgtctggca
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aatattaaggaagaggcagggttcaagaggagccatggggcactacgtcttagctgaacgtgagtgacac
gcagcctgcagactcactgtgggaaggagacaaaactagagactcaaagagggagtgcatttatgagctc
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